FIG. 1

FIG. 1A

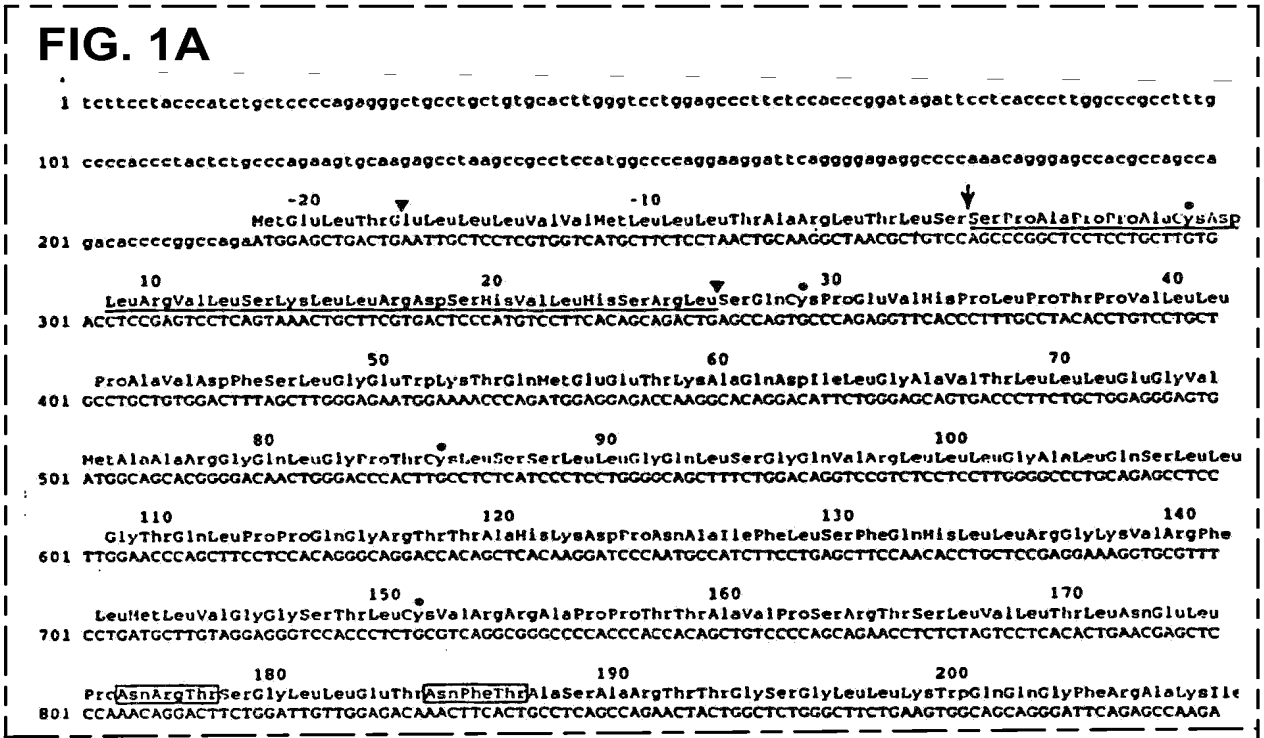


FIG. 1B

FIG. 1A

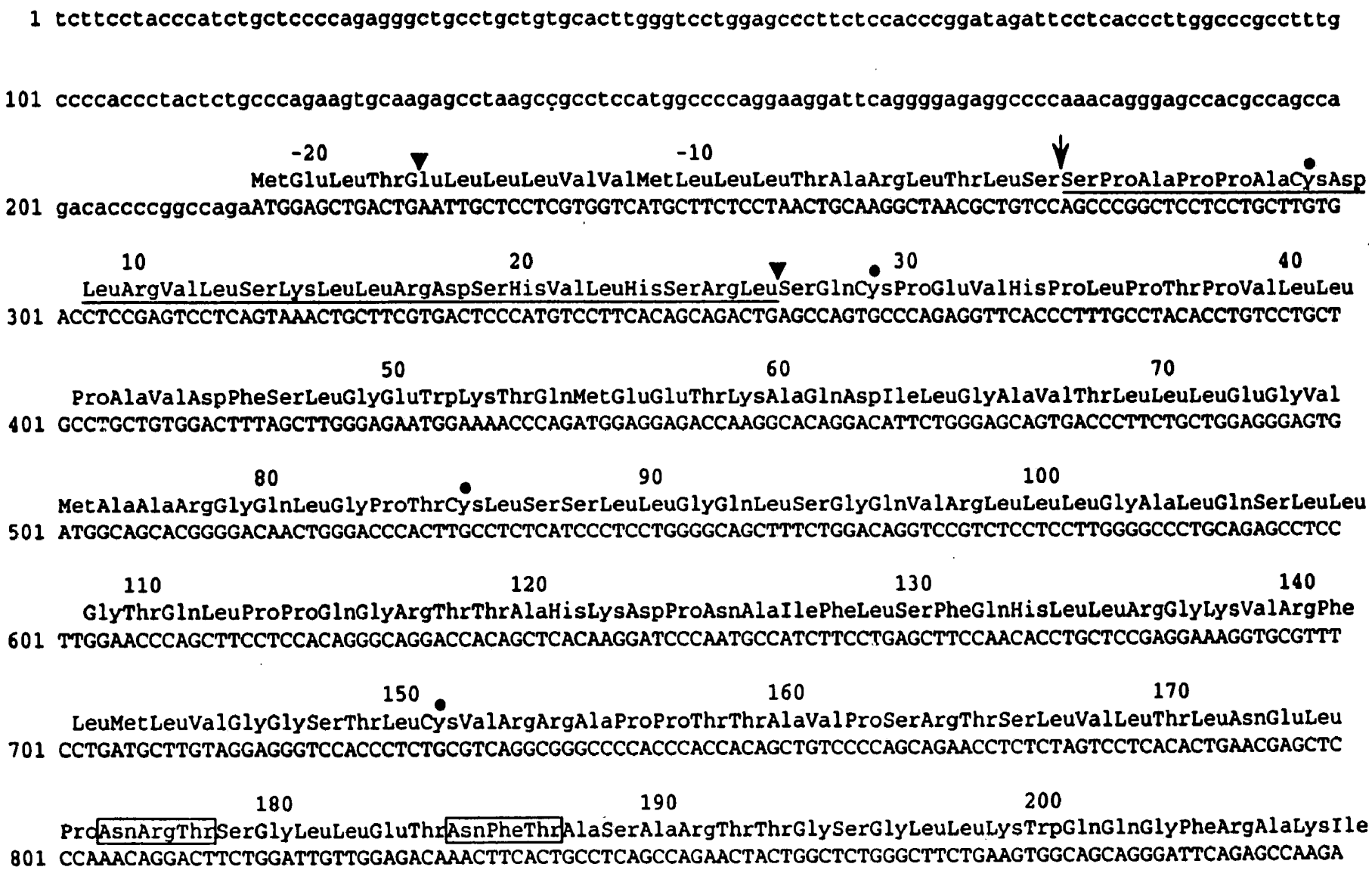

1 tcttcctacccatctgctccccagagggctgcctgctgtgcacttgggtcctggagcccttctccacccggatagattcctcacccttggcccgcctttg
101 ccccaccctactctgcccagaagtgcaagagcctaagccgcctccatggccccaggaaggattcaggggagaggccccaaacagggagccacgccagcca
-20
-10
MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
201 gacaccccggccagaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTG
10
20
30
40
LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
301 ACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT
50
60
70
ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG
80
90
100
MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
501 ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCC
110
120
130
140
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
601 TTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT
150
160
170
LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACCACAGCTGTCCCCAGCAGAACCTCTCTAGTCCTCACACTGAACGAGCTC
180
190
200
ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
801 CCAAACAGGACTTCTGGATTGTTGGAGACAAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTCAGAGCCAAGA

FIG. 1B


210 220 230 240
ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro
901 TTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTGGACCAAATCCCCGGATACCTGAACAGGATACACGAACTCTTGAATGGAACTCGTGGACTCTTTCC
250 260 270
GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
1001 TGGACCCTCACGCAGGACCCTAGGAGCCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCCTTCC
280 290 300
ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla
1101 CCAACCCATCCTCCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCACCCCTGTGGTCCAGCTCCACCCCCTGCTTCCTGACCCTTCTG
310 320 330
ProThrProThrProThrSerProLeuLeuAsnThrSerTyrThrHisSerGlnAsnLeuSerGlnGluGly
1201 CTCCAACGCCCACCCCTACCAGCCCTCTTCTAAACACATCCTACACCCACTCCCAGAATCTGTCTCAGGAAGGGTAAggttctcagacactgccgacatc
1301 agcattgtctcatgtacagctcccttccctgcagggcgcccctgggagacaactggacaagatttcctactttctcctgaaacccaaagccctggtaaaa
1401 gggatacacaggactgaaaagggaatcatttttcactgtacattataaaccttcagaagctatttttttaagctatcagcaatactcatcagagcagcta
1501 gctctttggtctattttctgcagaaatttgcaactcactgattctctacatgctctttttctgtgataactctgcaaaggcctgggctggcctggcagtt
1601 gaacagagggagagactaaccttgagtcagaaaacagagaaagggtaatttcctttgcttcaaattcaaggccttccaacgcccccatcccctttactat
1701 cattctcagtgggactctgatcccatattcttaacagatctttactcttgagaaatgaataagctttctctcagaaaaaaaaaaaaaaaaaaaaa

FIG. 2

FIG. 2A

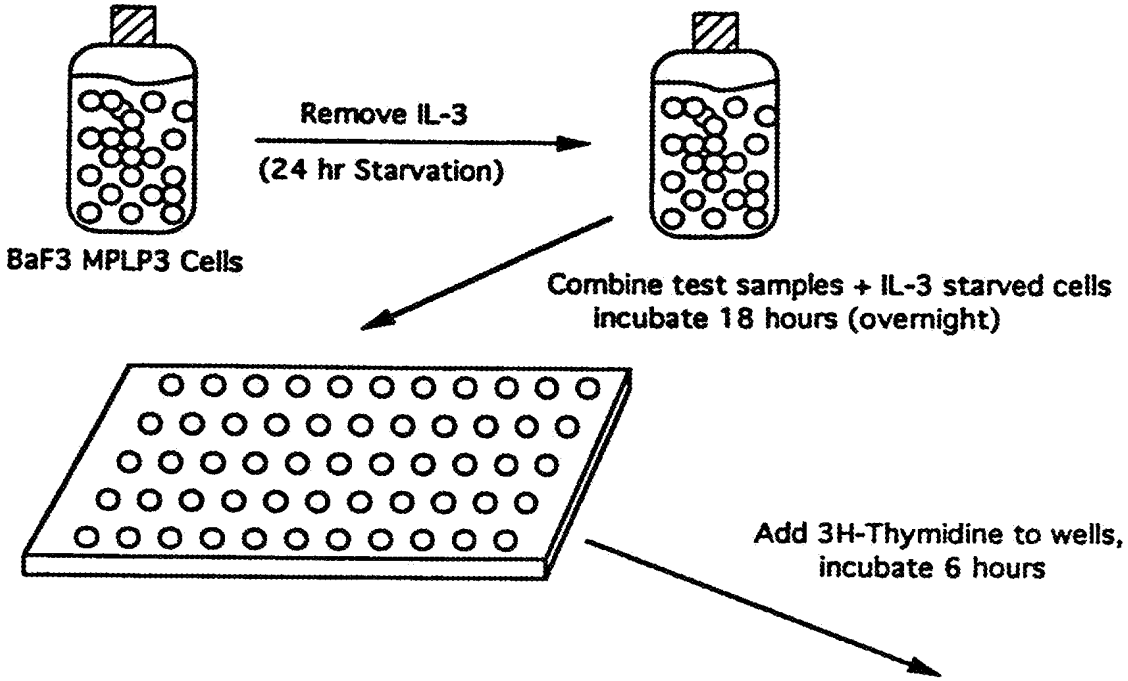


FIG. 2B

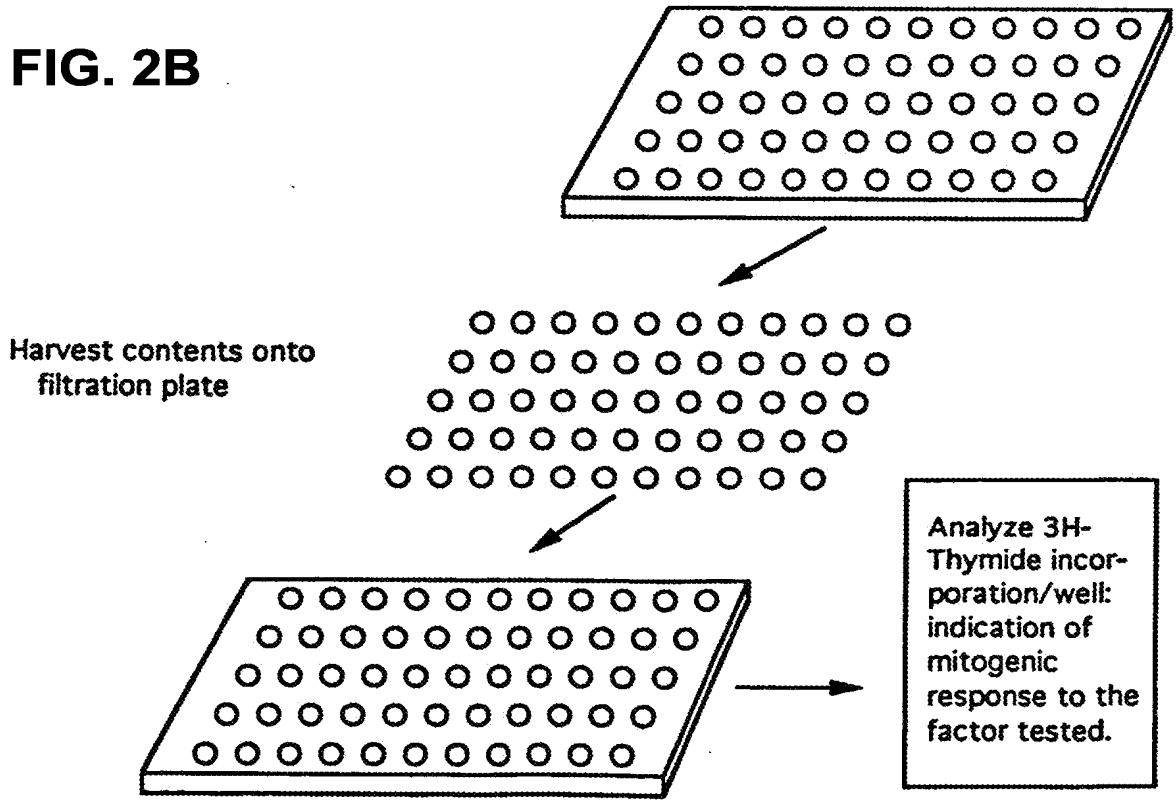
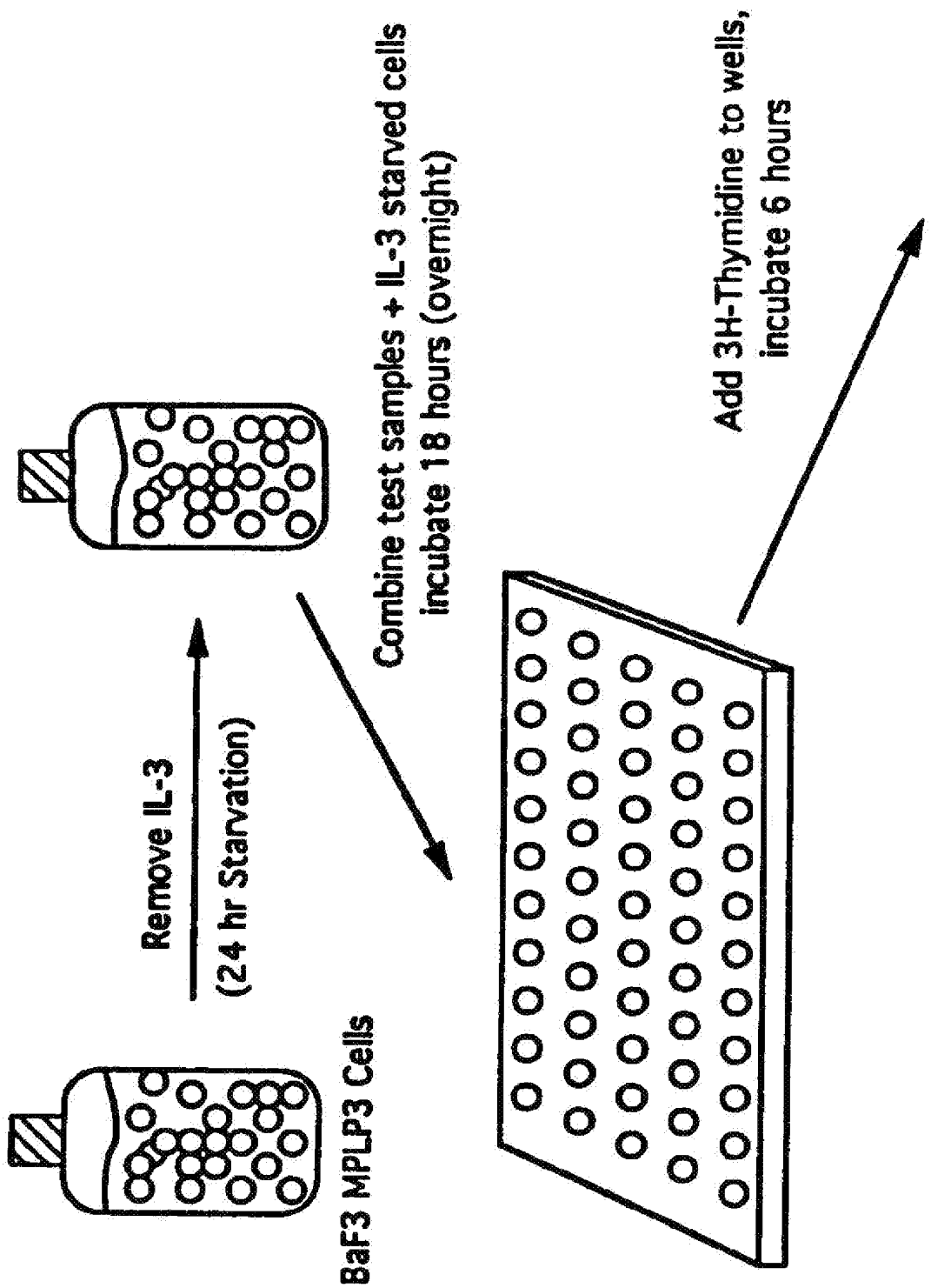


FIG. 2A


BaF3 MPLP3 Cells
Remove IL-3
(24 hr Starvation)
Combine test samples + IL-3 starved cells
incubate 18 hours (overnight)
Add 3H-Thymidine to wells,
incubate 6 hours

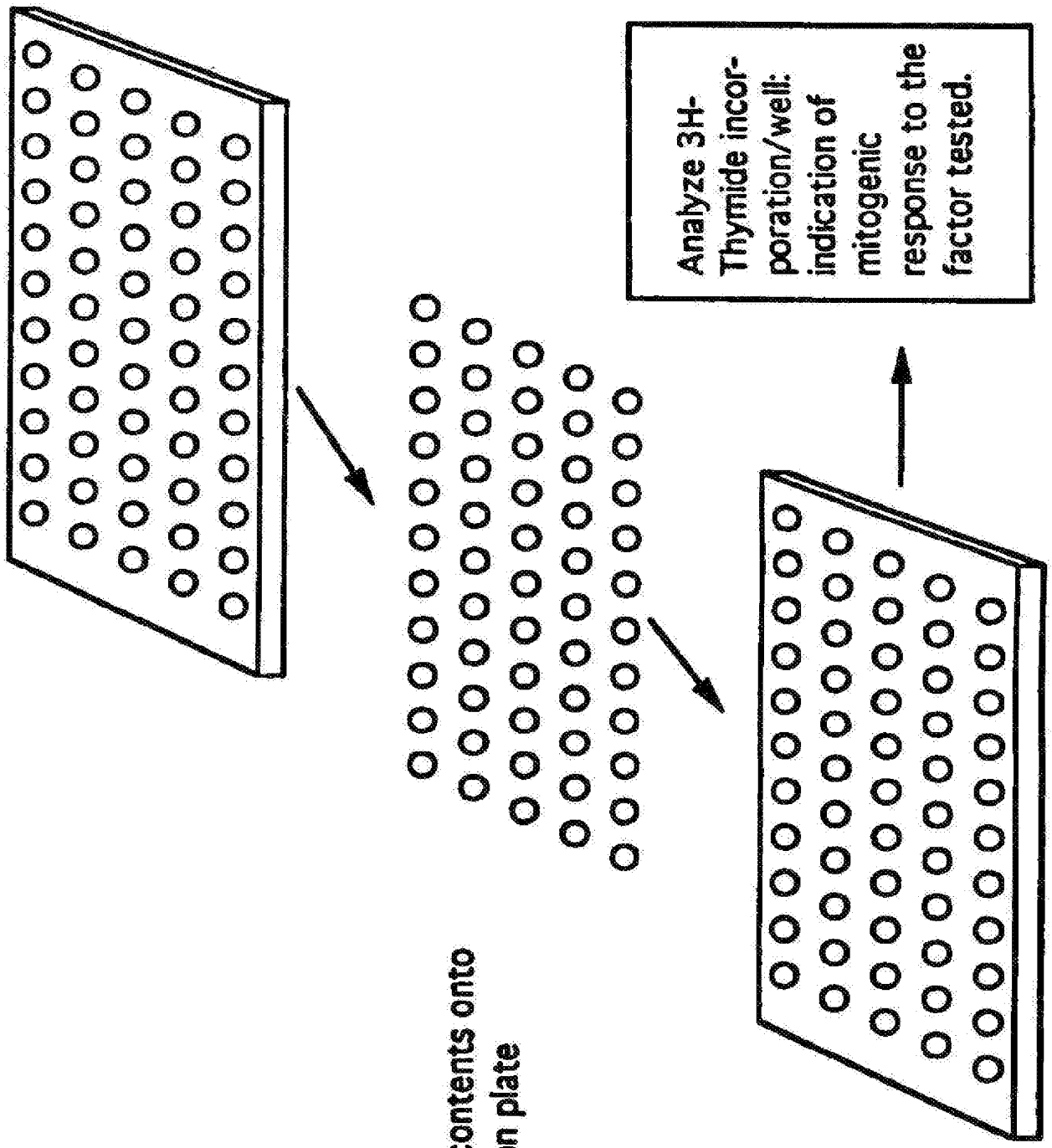

Harvest contents onto filtration plate
Analyze 3H-Thymide incorporation/well: indication of mitogenic response to the factor tested.

FIG. 2B

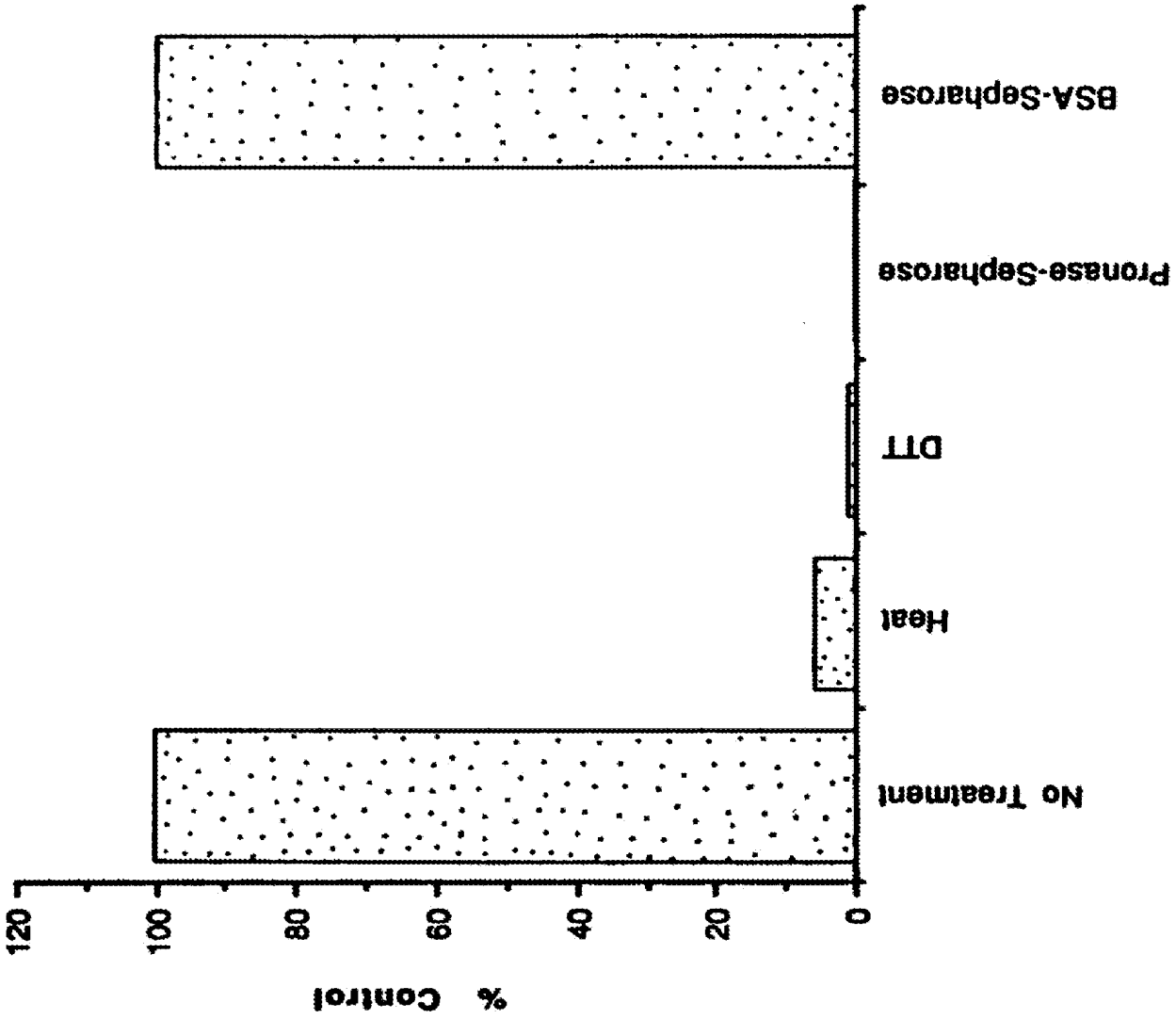

No Treatment
Heat
DTT
Pronase-Sepharose
BSA-Sepharose
% Control
120
100
80
60
40
20
0

FIG. 3

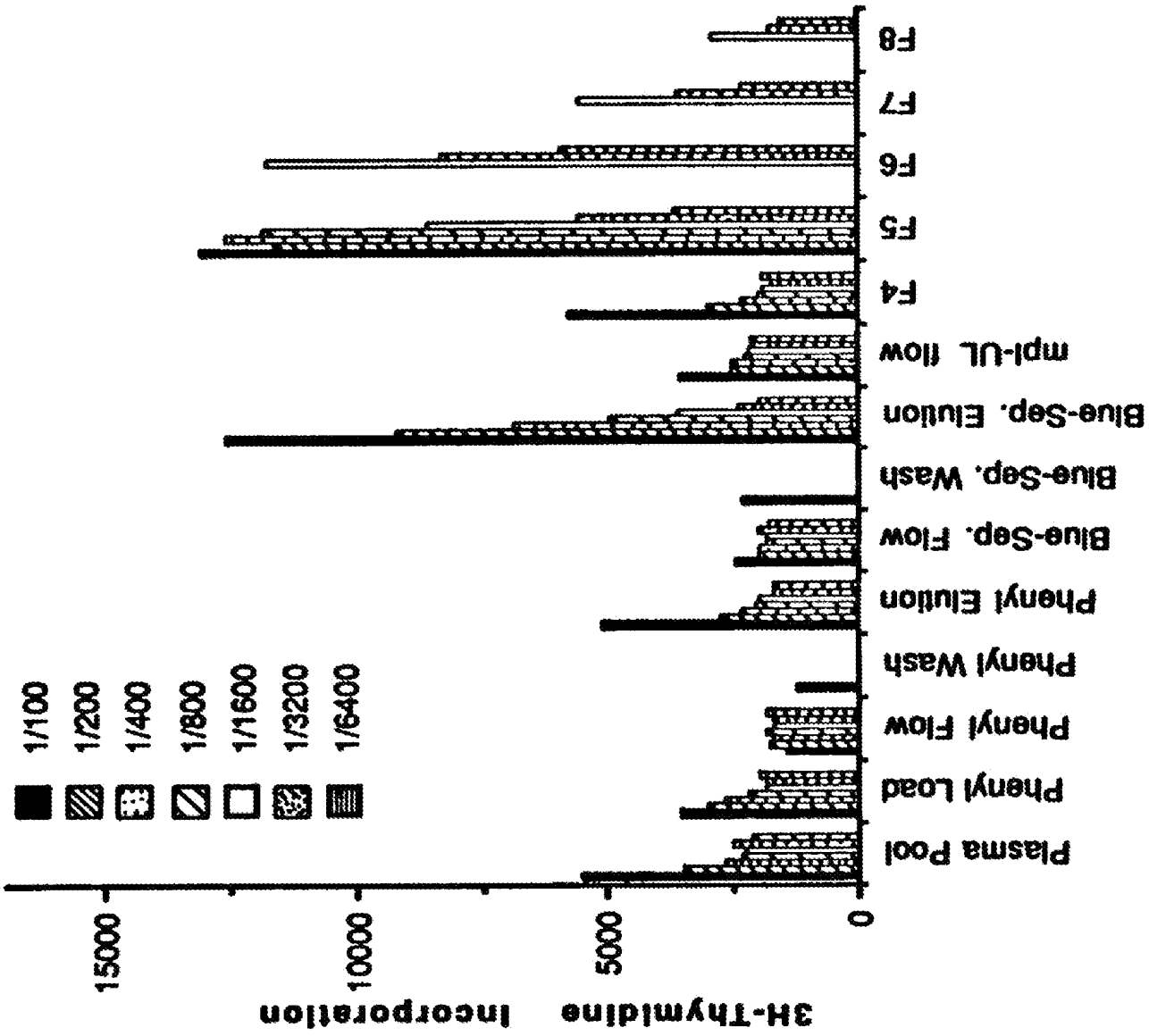

3H-Thymidine Incorporation
15000
10000
5000
0
1/100
1/200
1/400
1/800
1/1600
1/3200
1/6400
Plasma Pool
Phenyl Load
Phenyl Flow
Phenyl Wash
Phenyl Elution
Blue-Sep. Flow
Blue-Sep. Wash
Blue-Sep. Elution
mpl-UL flow
F4
F5
F6
F7
F8

FIG. 4

FIG. 5

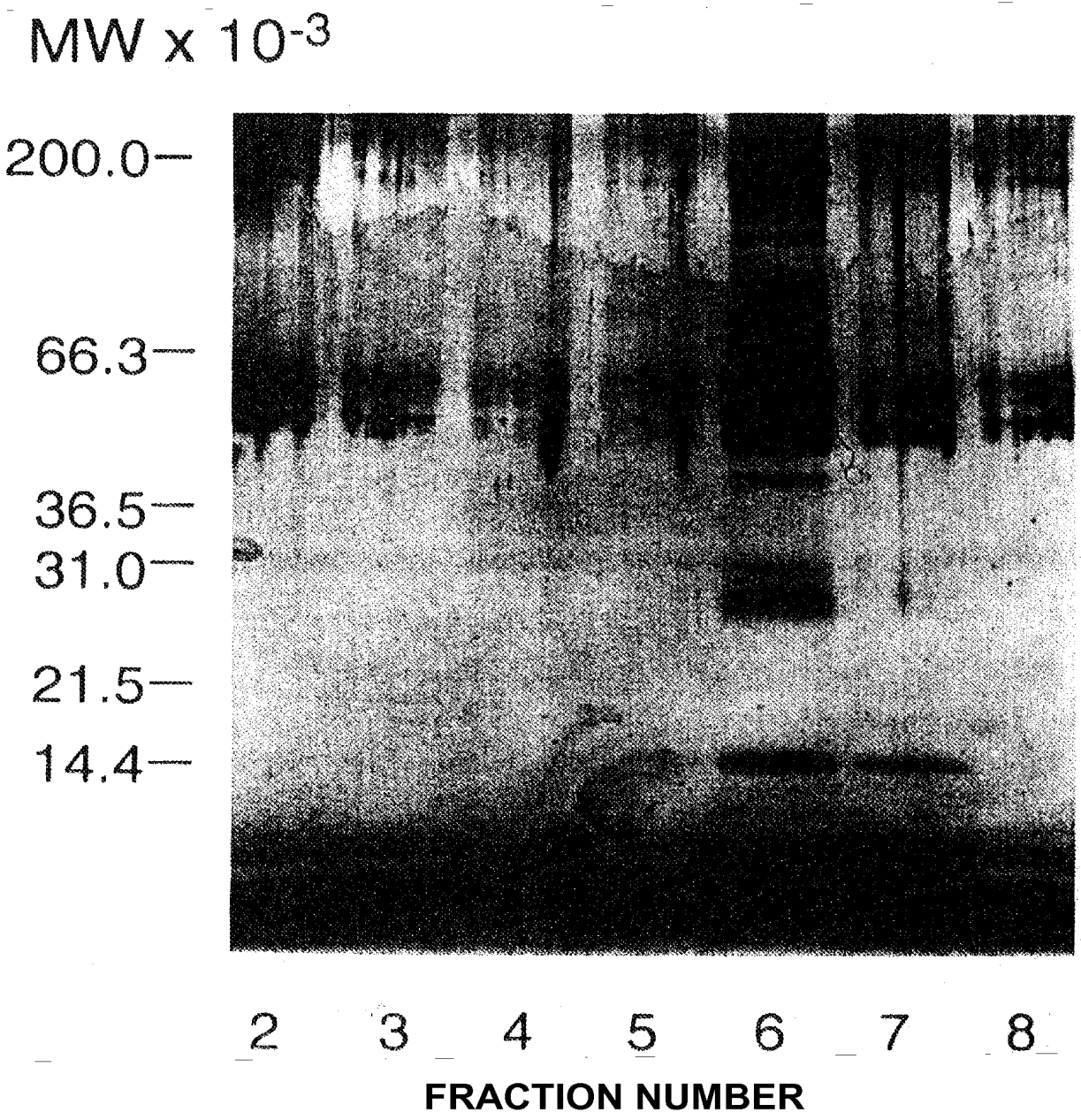


FIG.6

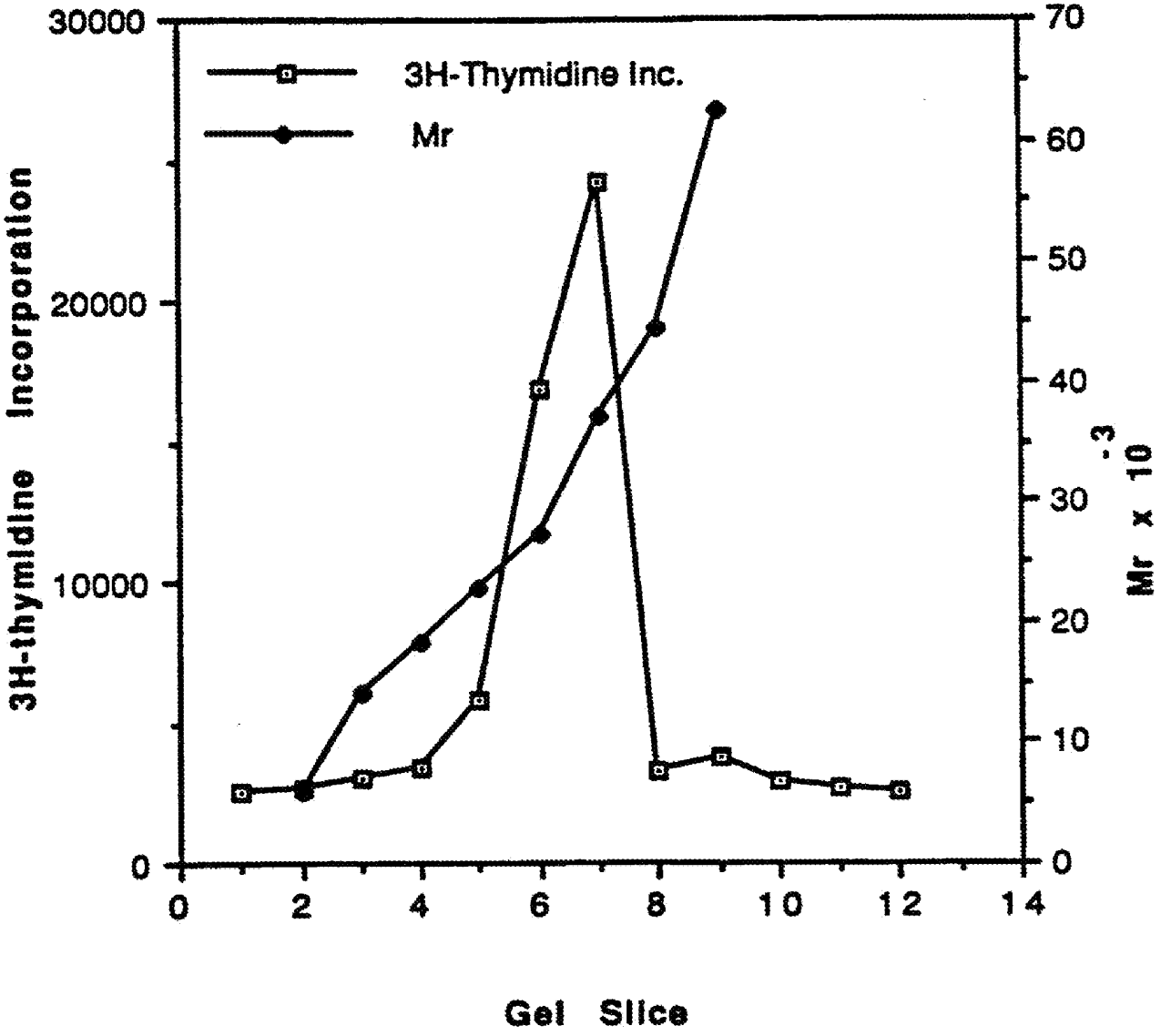
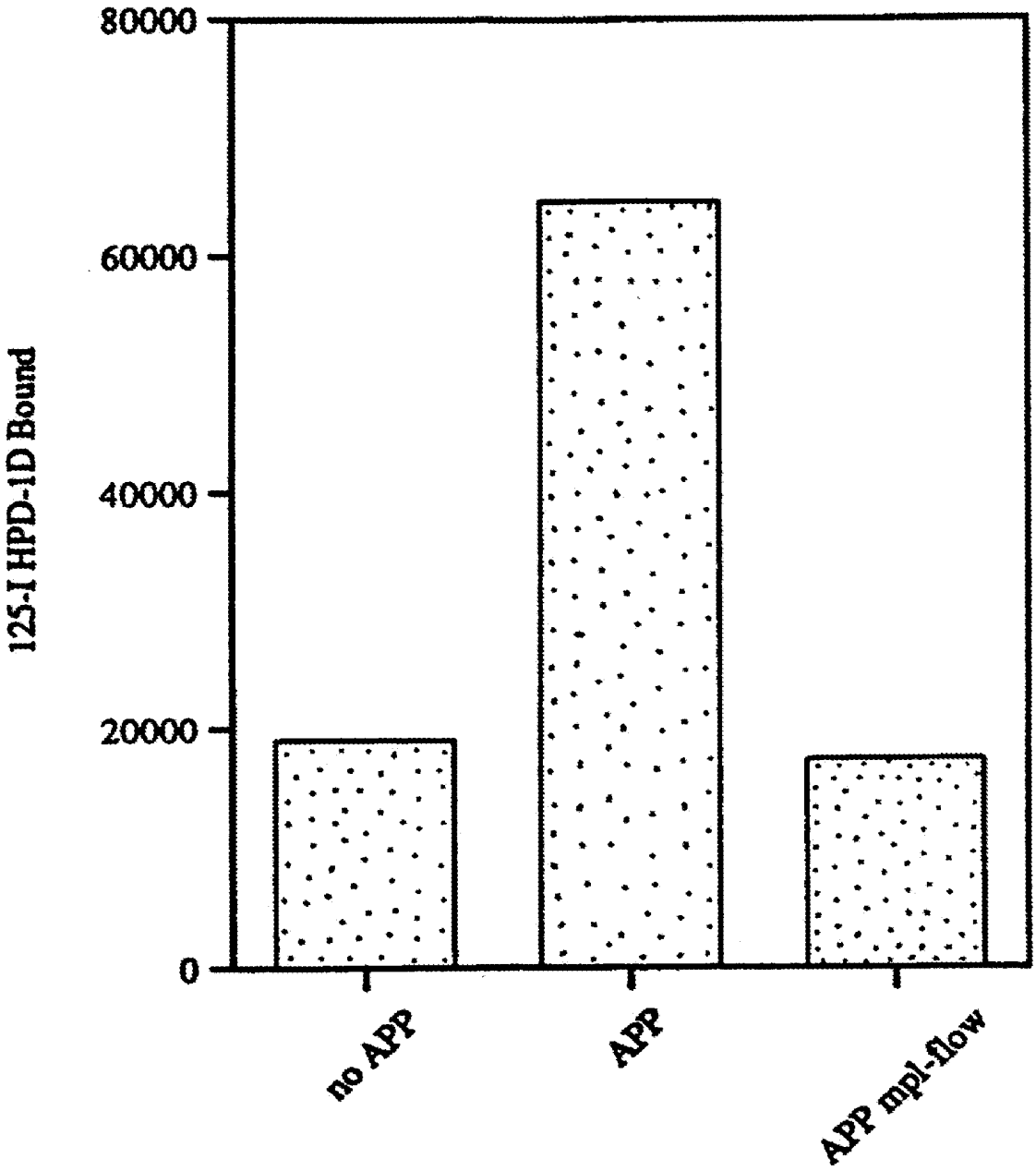

3H-Thymidine Inc.
Mr
3H-thymidine Incorporation
Mr x 10 .3
Gel Slice
30000
20000
10000
0
70
60
50
40
30
20
10
0
0
2
4
6
8
10
12
14

FIG. 7


80000
60000
40000
20000
0
125-I HPD-1D Bound
no APP
APP
APP mpl-flow

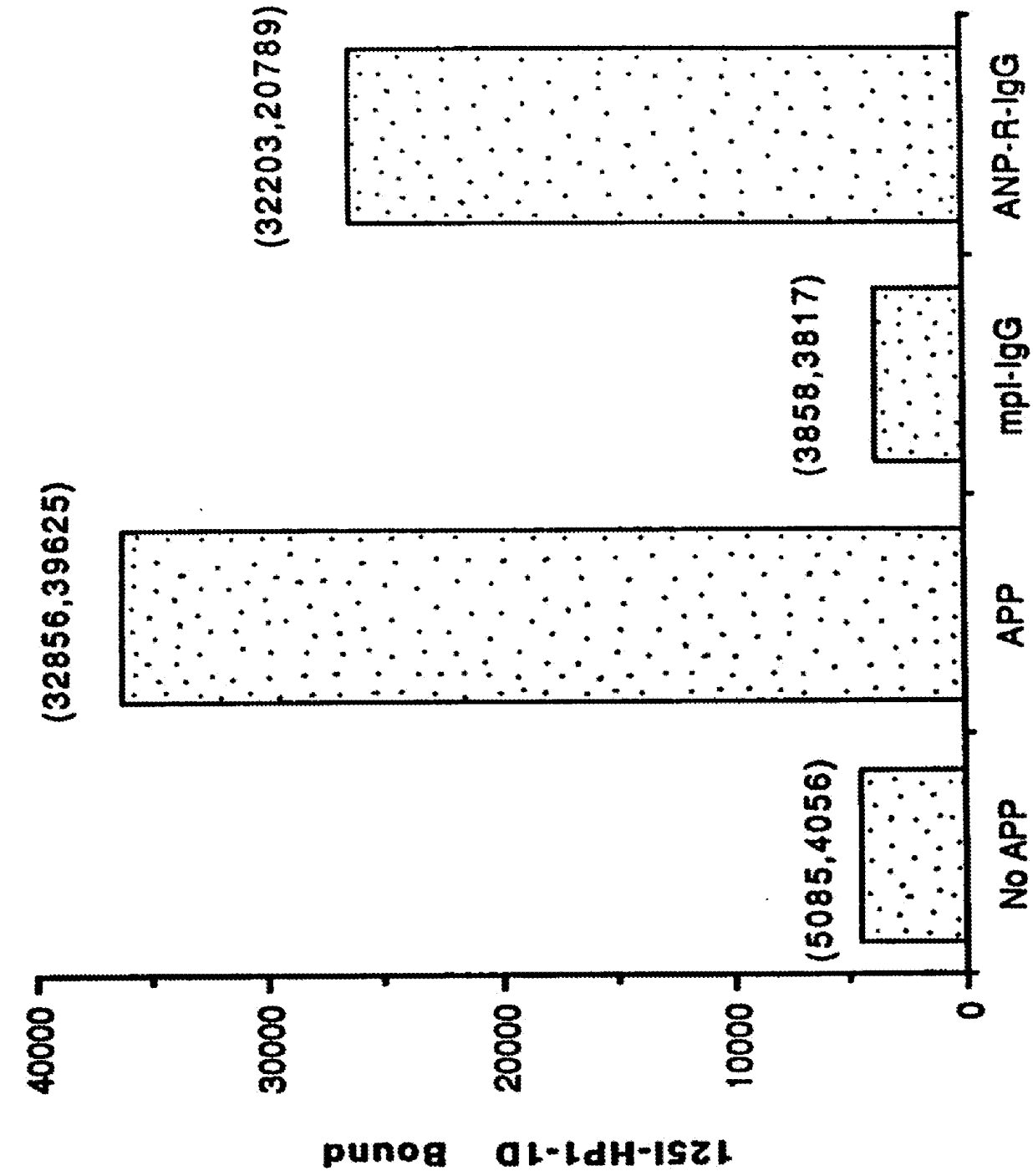

125I-HP1-1D Bound
40000
30000
20000
10000
0
(32856,39625)
(32203,20789)
(5085,4056)
(3858,3817)
No APP
APP
mpl-IgG
ANP-R-IgG

FIG. 8

FIG. 9

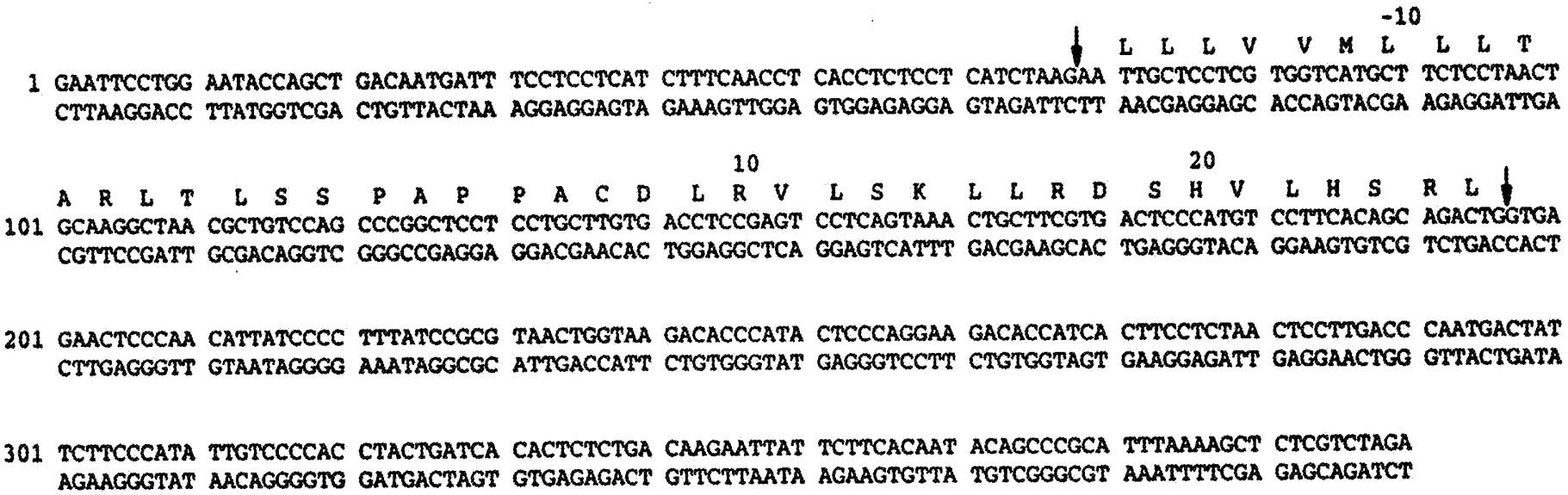

-10
L L L V V M L L L T
1 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT
CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA
10
20
A R L T L S S P A P P A C D L R V L S K L L R D S H V L H S R L
101 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT
201 GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT
CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA
301 TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT

FIG. 10

FIG. 11

FIG.11A

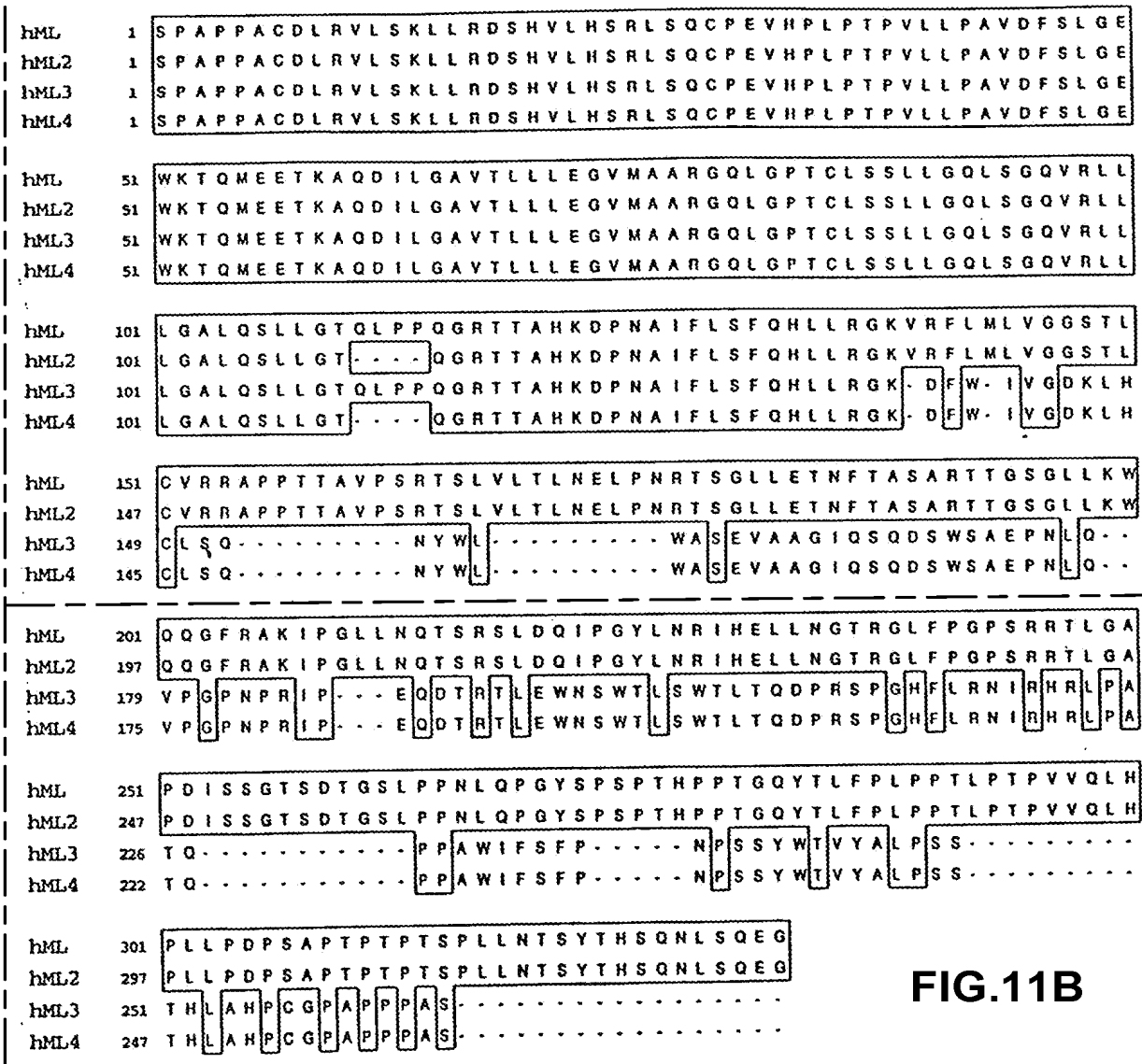


FIG.11B

FIG. 11A

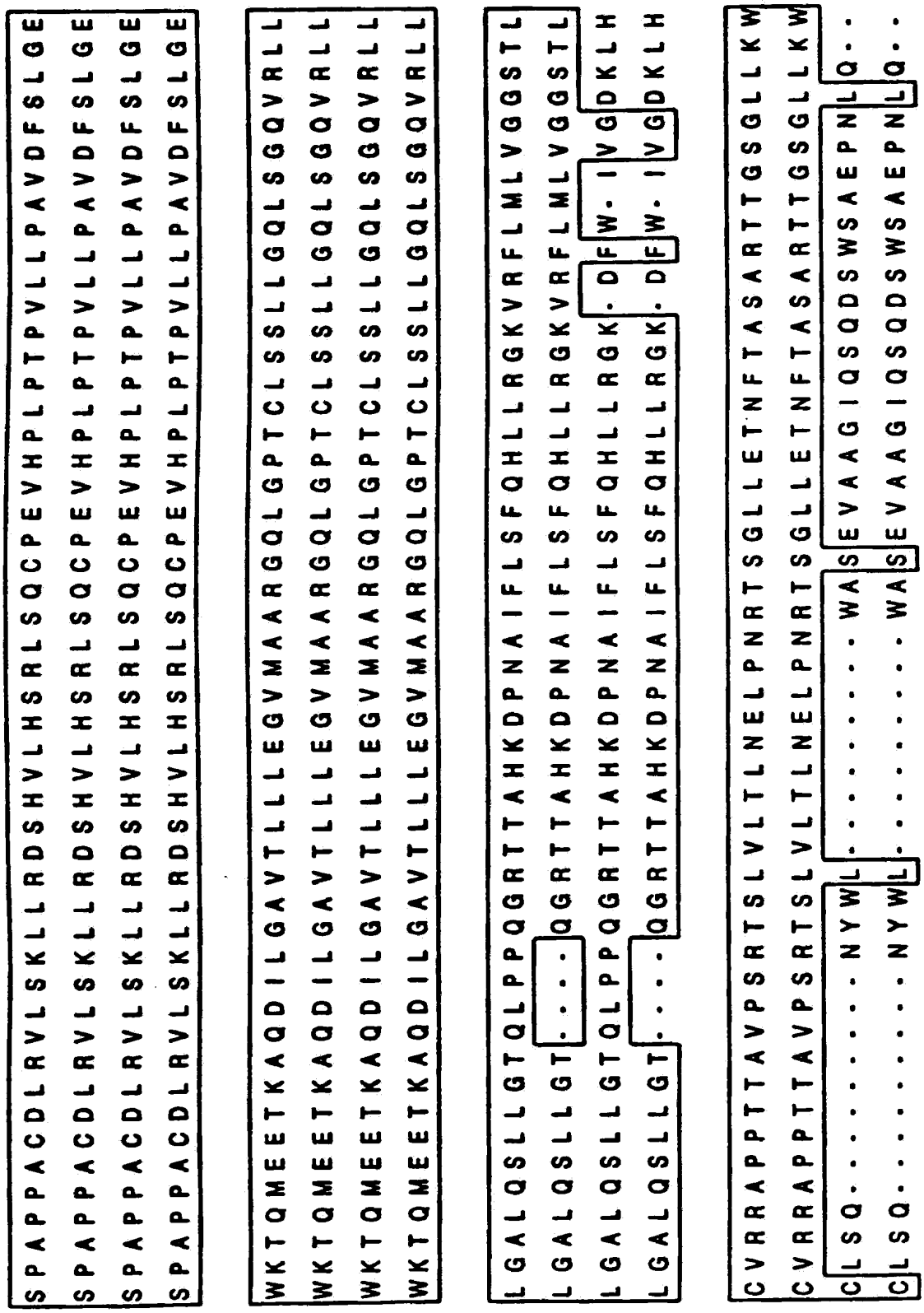

hML 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML2 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML3 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML4 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML2 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML3 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML4 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML2 101 LGALQSLLGT----QGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML3 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK-DFW-IVGDKLH
hML4 101 LGALQSLLGT----QGRTTAHKDPNAIFLSFQHLLRGK-DFW-IVGDKLH
hML 151 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML2 147 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML3 149 CLSQ----------NYWL----------WASEVAAGIQSQDSWSAEPNLQ--
hML4 145 CLSQ----------NYWL----------WASEVAAGIQSQDSWSAEPNLQ--

FIG. 11B

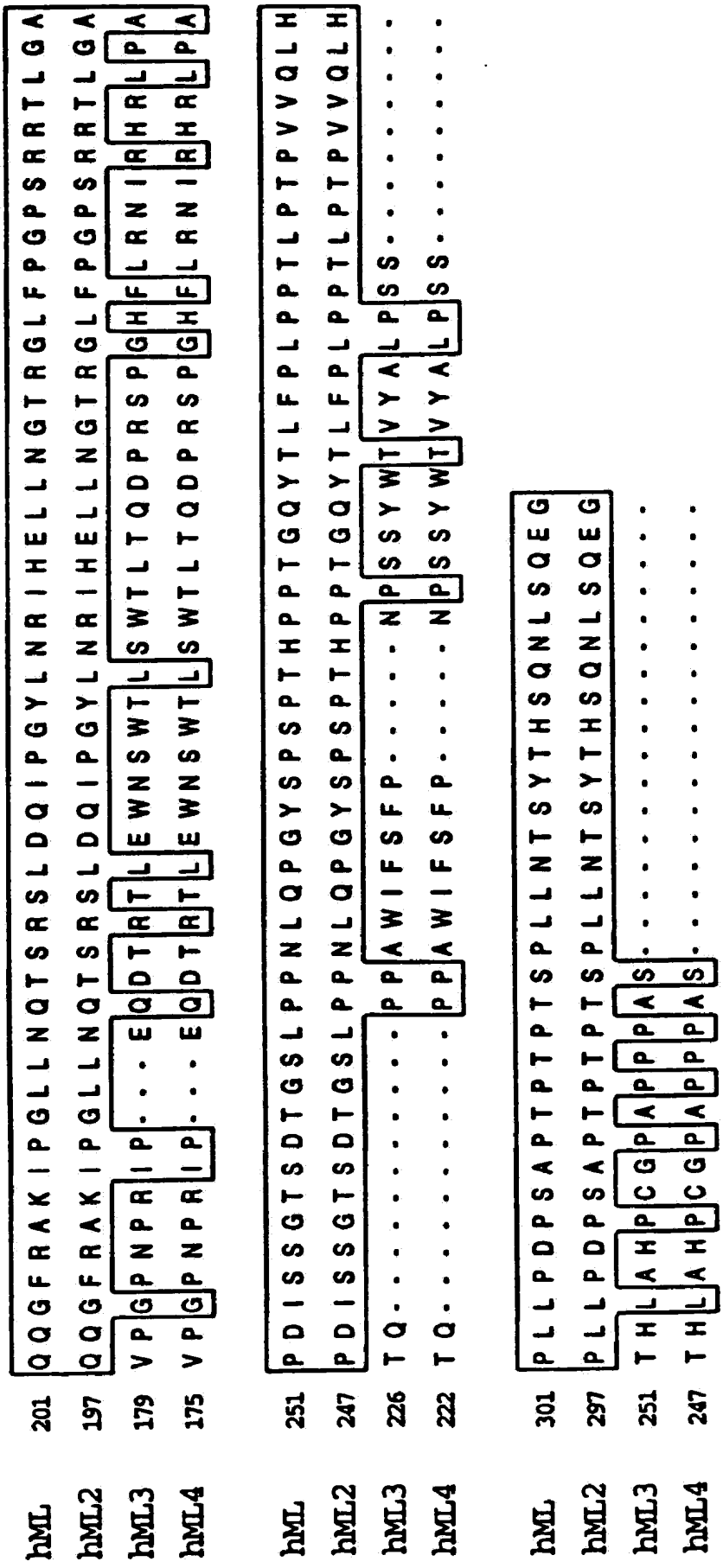

hML 201 QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML2 197 QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML3 179 VPGPNPRIP---EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA
hML4 175 VPGPNPRIP---EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA
hML 251 PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML2 247 PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML3 226 TQ----------PPAWIFSFP-----NPSSYWTVYALPSS---------
hML4 222 TQ----------PPAWIFSFP-----NPSSYWTVYALPSS---------
hML 301 PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML2 297 PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML3 251 THLAHPCGPAPPPAS----------
hML4 247 THLAHPCGPAPPPAS----------

FIG. 12A

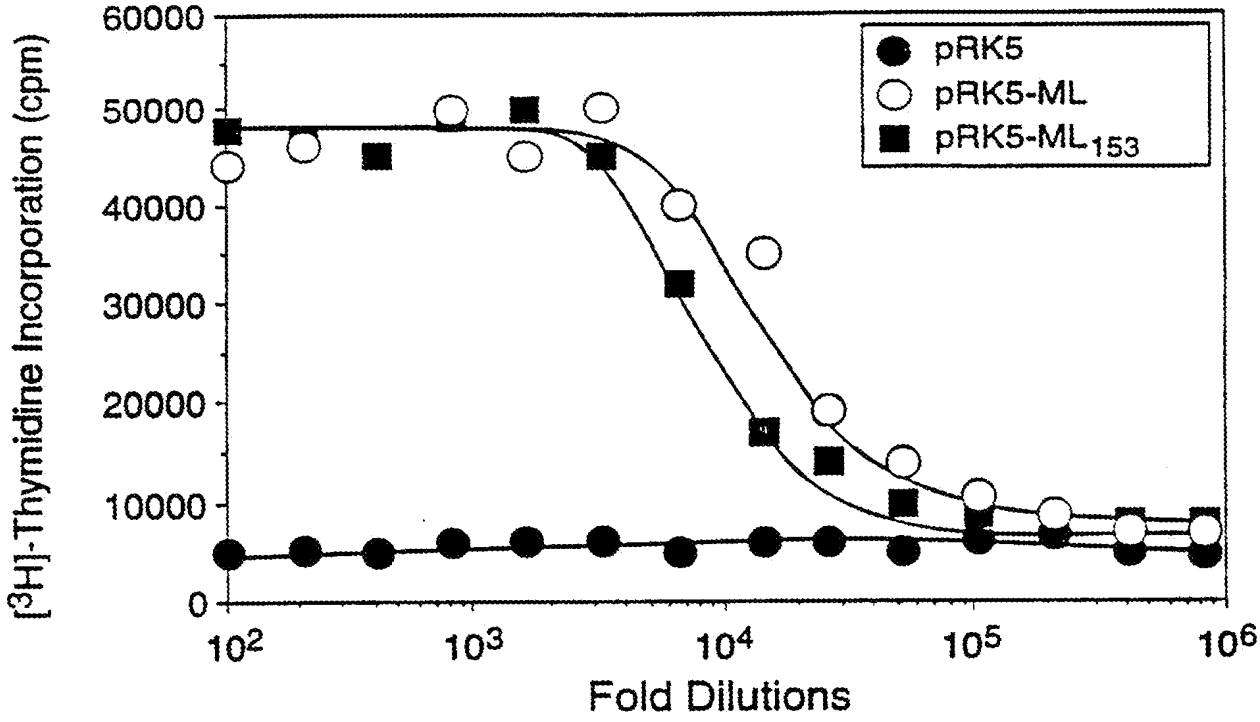


FIG. 12B

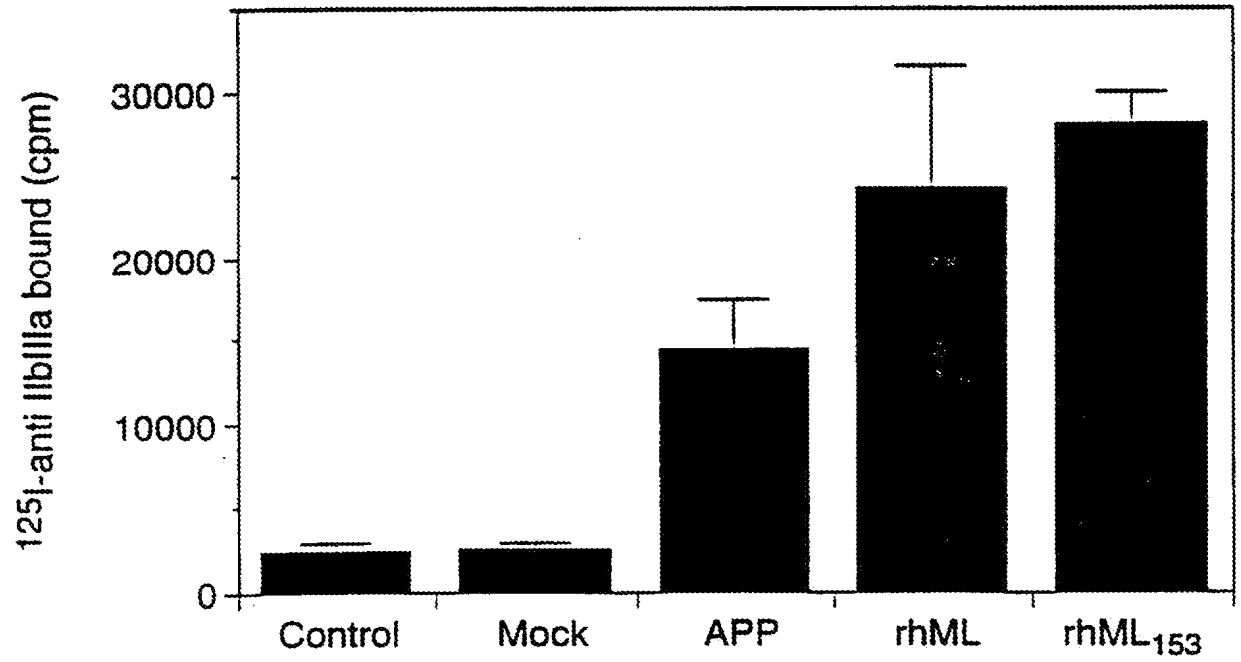


FIG. 12D

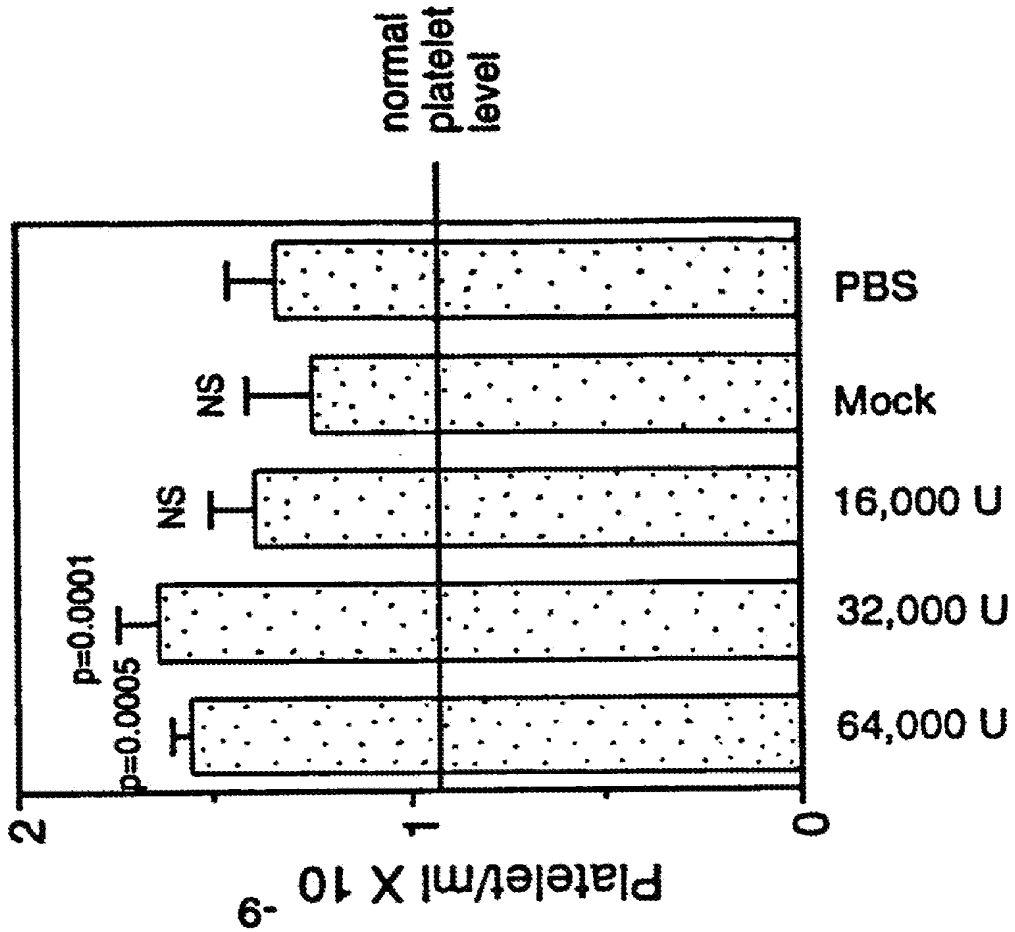
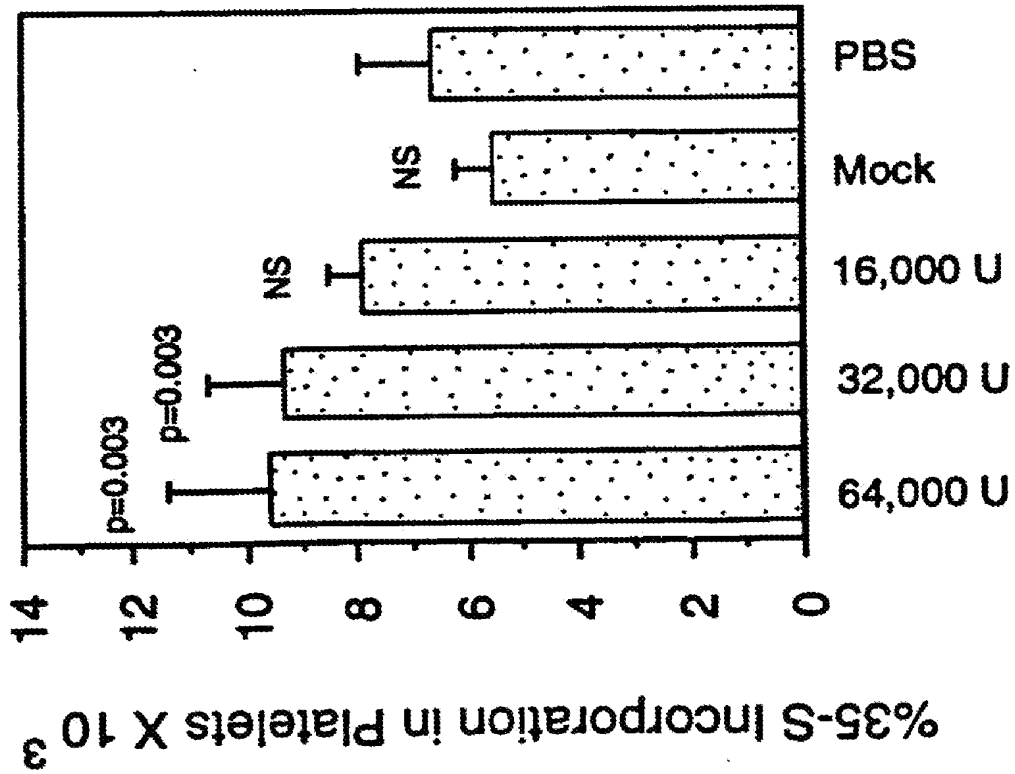


FIG. 12C



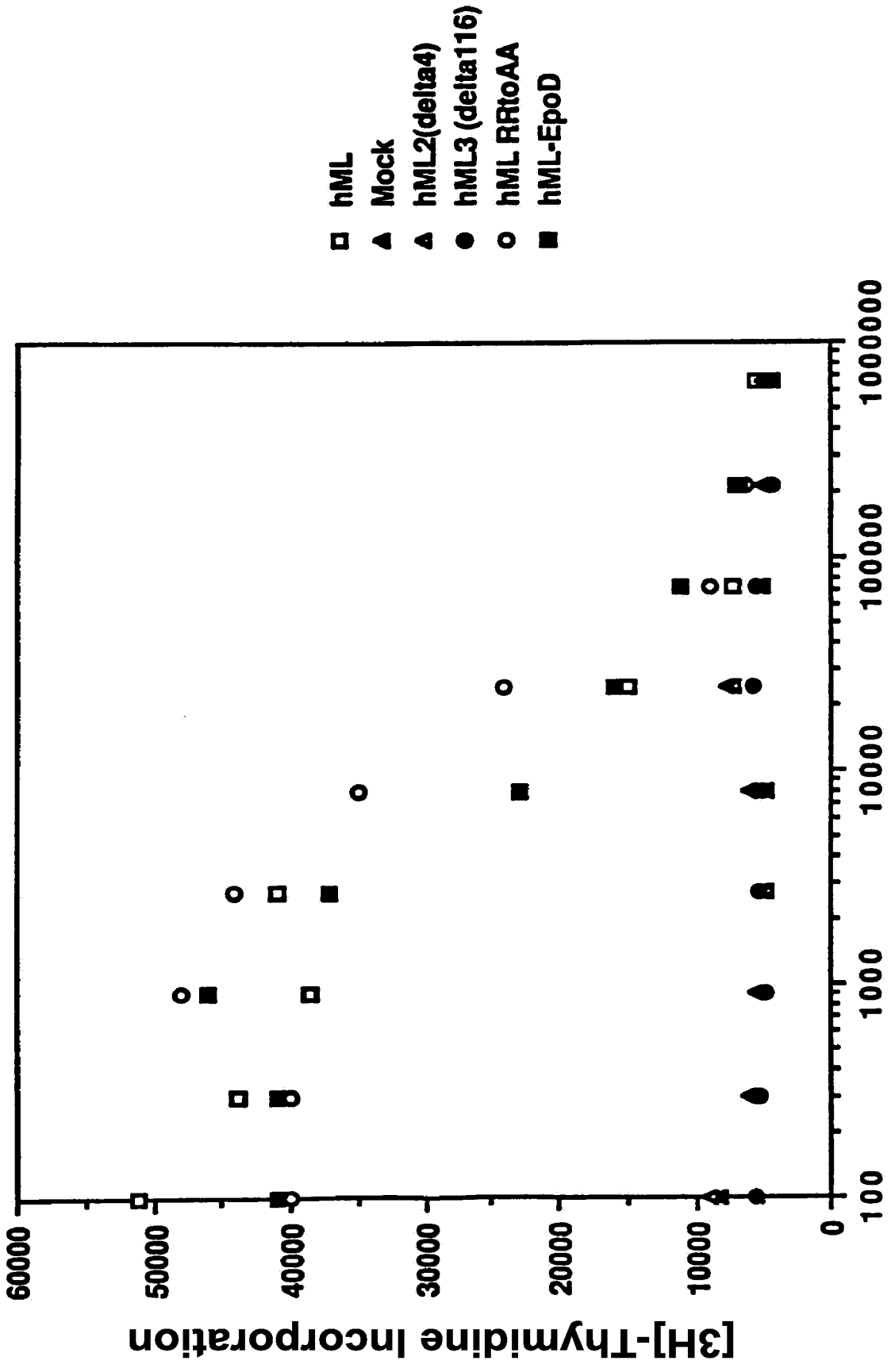

hML
Mock
hML2(delta4)
hML3 (delta116)
hML RRtoAA
hML-EpoD
[3H]-Thymidine Incorporation
60000
50000
40000
30000
20000
10000
0
100
1000
10000
100000
1000000
Fold Dilution

FIG. 13

FIG. 14

FIG.14A

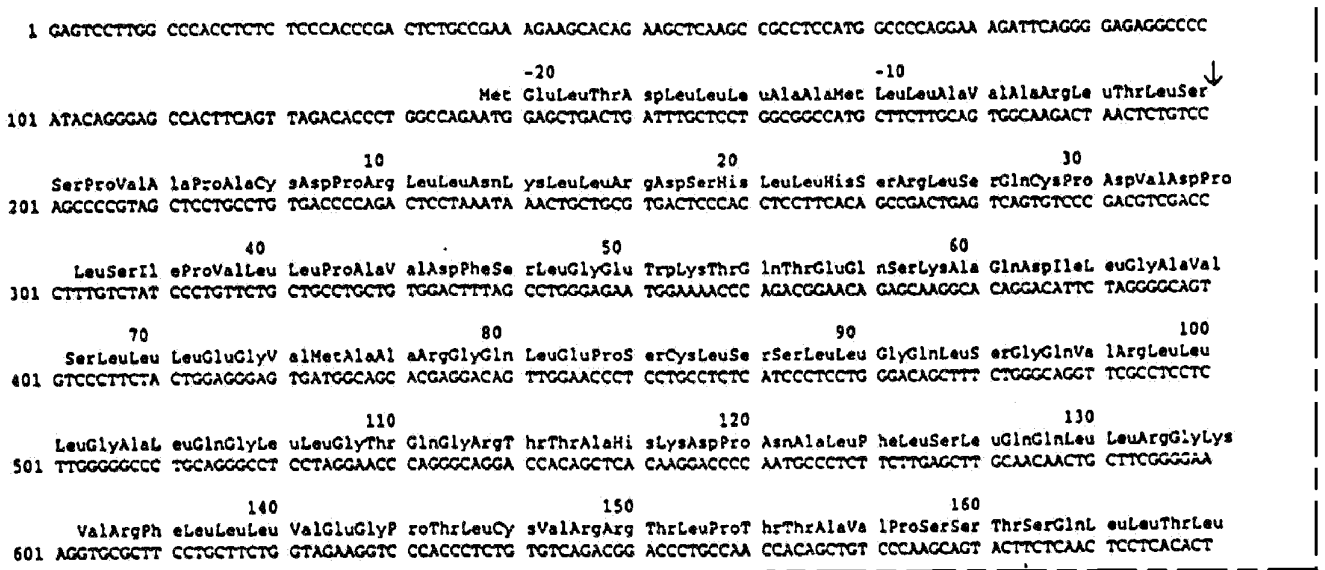


FIG.14B

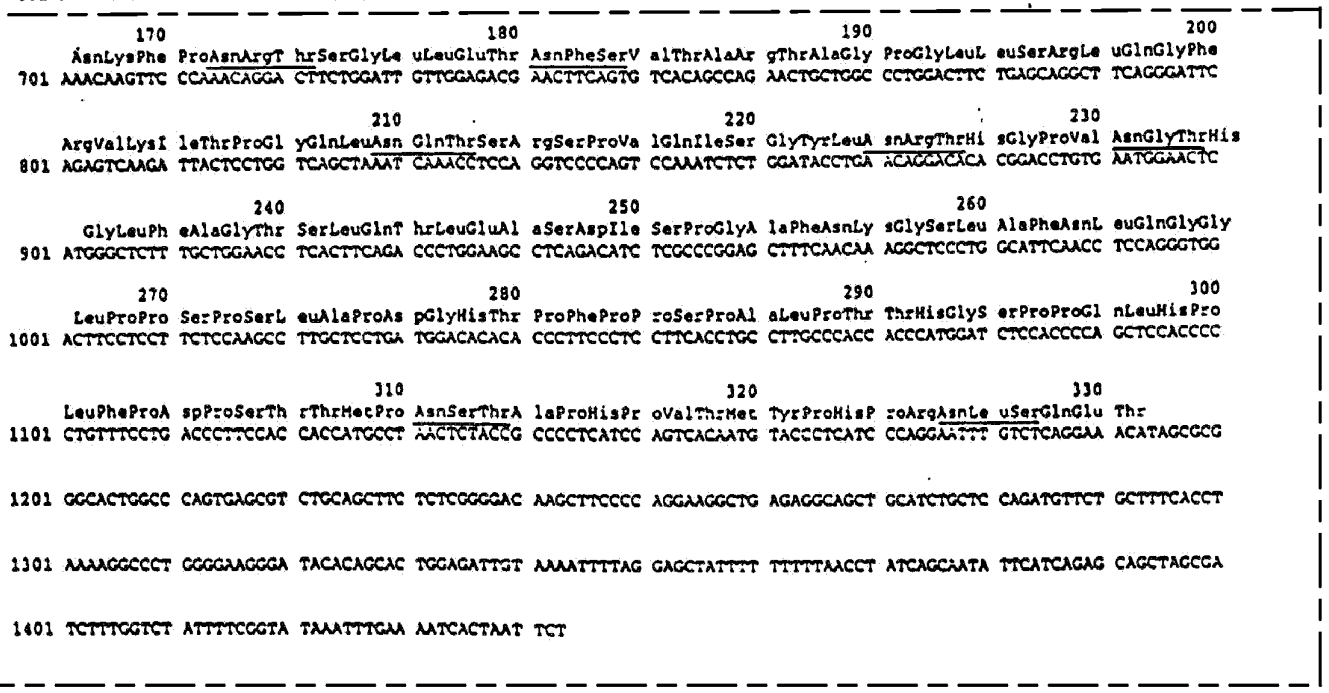


FIG. 14A

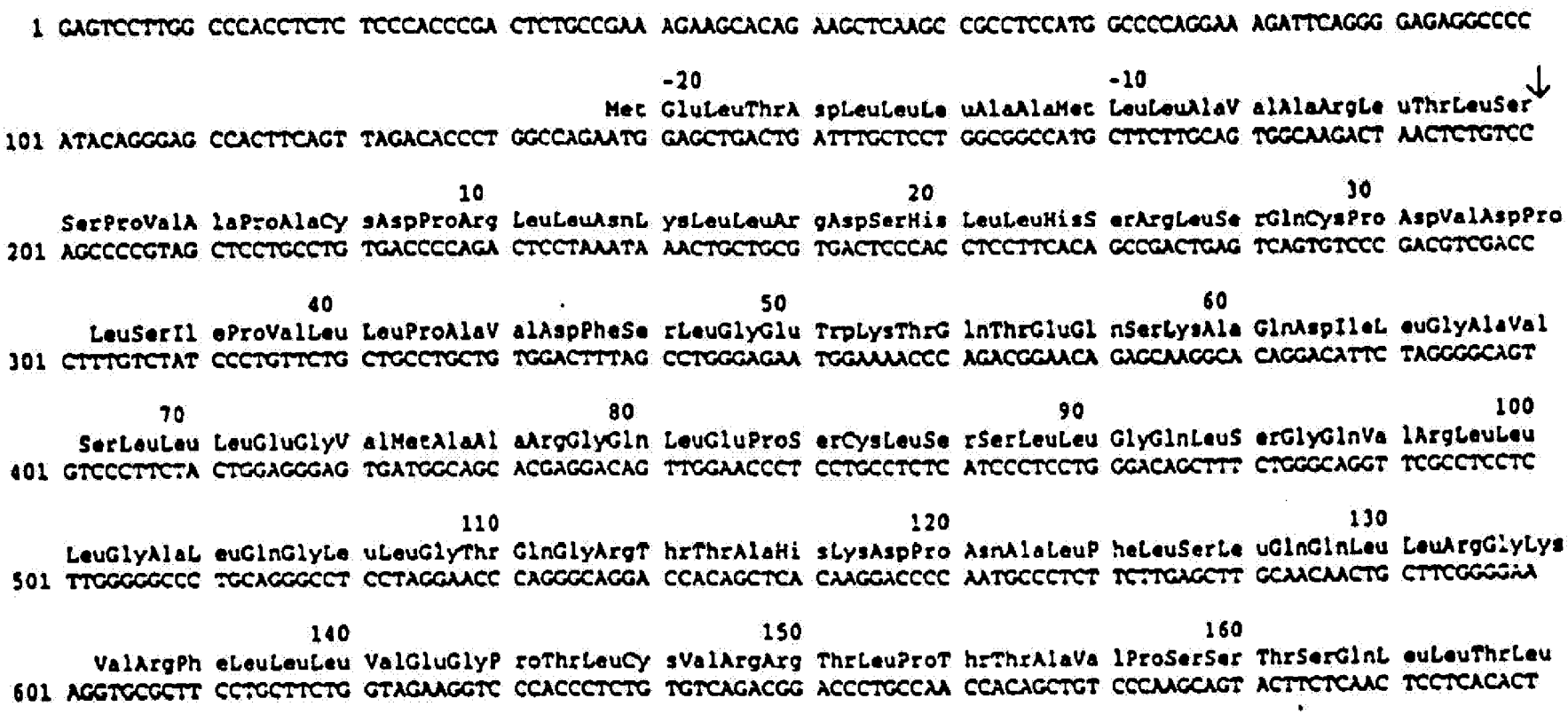

1 GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC
-20
-10
Met GluLeuThrA spLeuLeuLe uAlaAlaMet LeuLeuAlaV alAlaArgLe uThrLeuSer
101 ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC
10
20
30
SerProValA laProAlaCy sAspProArg LeuLeuAsnL ysLeuLeuAr gAspSerHis LeuLeuHisS erArgLeuSe rGlnCysPro AspValAspPro
201 AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC
40
50
60
LeuSerIl eProValLeu LeuProAlaV alAspPheSe rLeuGlyGlu TrpLysThrG lnThrGluGl nSerLysAla GlnAspIleL euGlyAlaVal
301 CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT
70
80
90
100
SerLeuLeu LeuGluGlyV alMetAlaAl aArgGlyGln LeuGluProS erCysLeuSe rSerLeuLeu GlyGlnLeuS erGlyGlnVa lArgLeuLeu
401 GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC
110
120
130
LeuGlyAlaL euGlnGlyLe uLeuGlyThr GlnGlyArgT hrThrAlaHi sLysAspPro AsnAlaLeuP heLeuSerLe uGlnGlnLeu LeuArgGlyLys
501 TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACTG CTTCGGGGAA
140
150
160
ValArgPh eLeuLeuLeu ValGluGlyP roThrLeuCy sValArgArg ThrLeuProT hrThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
601 AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT

FIG. 14B

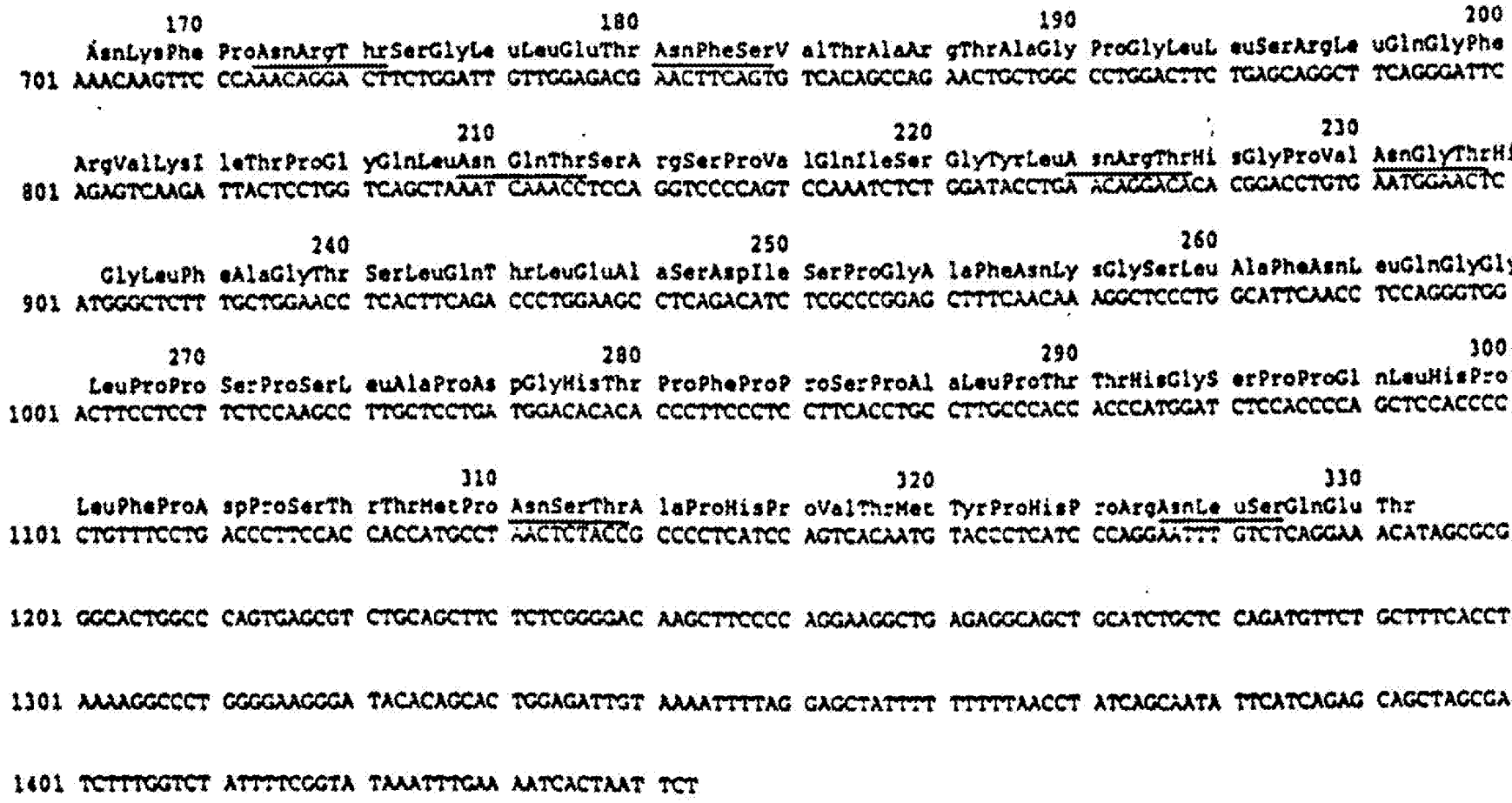

170 180 190 200
AsnLysPhe ProAsnArgT hrSerGlyLe uLeuGluThr AsnPheSerV alThrAlaAr gThrAlaGly ProGlyLeuL euSerArgLe uGlnGlyPhe
701 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC
210 220 230
ArgValLysI leThrProGl yGlnLeuAsn GlnThrSerA rgSerProVa lGlnIleSer GlyTyrLeuA snArgThrHi sGlyProVal AsnGlyThrHis
801 AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAACTC
240 250 260
GlyLeuPh eAlaGlyThr SerLeuGlnT hrLeuGluAl aSerAspIle SerProGlyA laPheAsnLy sGlySerLeu AlaPheAsnL euGlnGlyGly
901 ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG
270 280 290 300
LeuProPro SerProSerL euAlaProAs pGlyHisThr ProPheProP roSerProAl aLeuProThr ThrHisGlyS erProProGl nLeuHisPro
1001 ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC CTTCACCTGC CTTGCCCACC ACCCATGGAT CTCCACCCCA GCTCCACCCC
310 320 330
LeuPheProA spProSerTh rThrMetPro AsnSerThrA laProHisPr oValThrMet TyrProHisP roArgAsnLe uSerGlnGlu Thr
1101 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG
1201 GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT
1301 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG GAGCTATTTT TTTTTAACCT ATCAGCAATA TTCATCAGAG CAGCTAGCGA
1401 TCTTTGGTCT ATTTTCCGTA TAAATTTGAA AATCACTAAT TCT

FIG. 15

FIG.15A

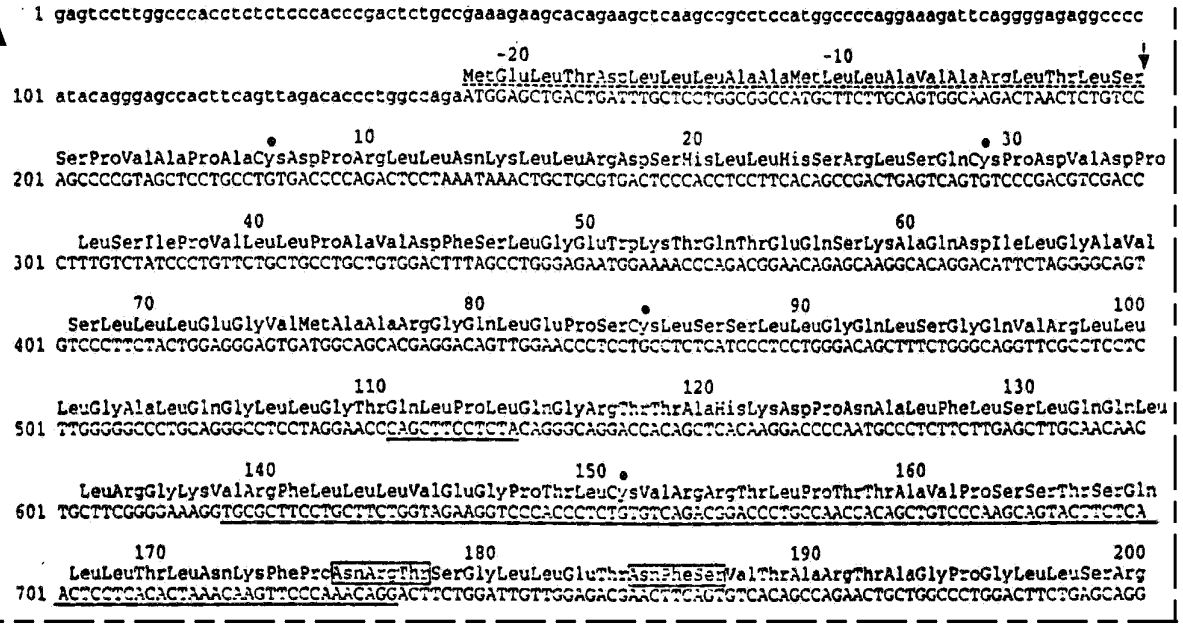


FIG.15B

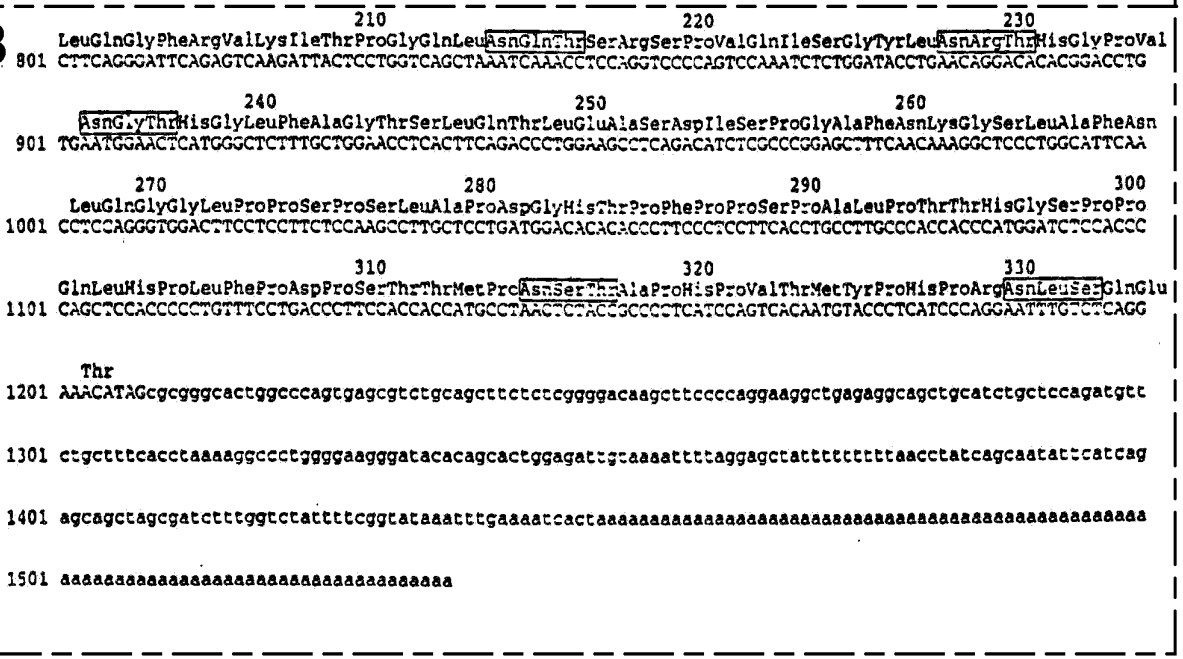


FIG. 15A

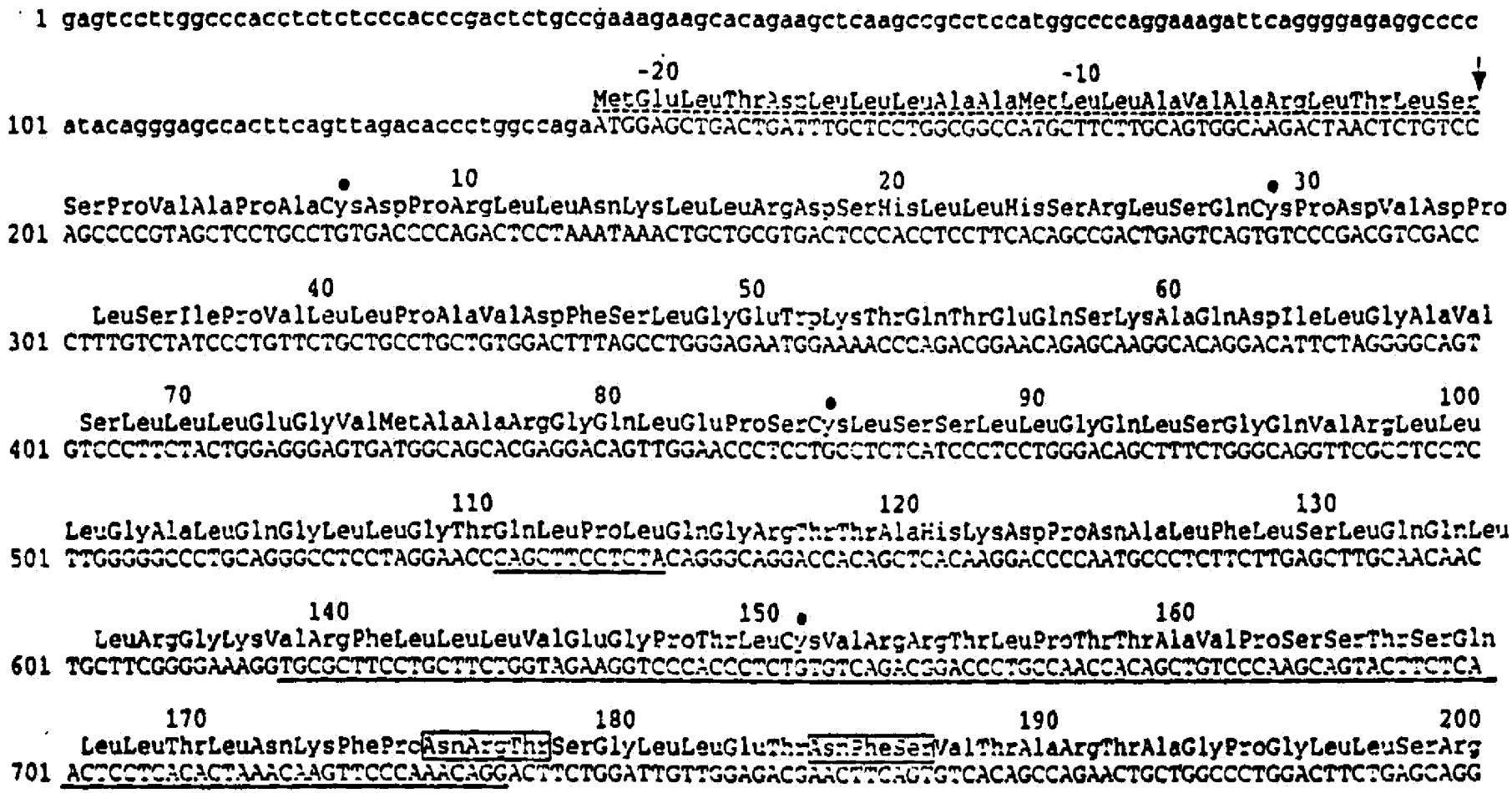

1 gagtccttggcccacctctctcccacccgactctgccgaaagaagcacagaagctcaagccgcctccatggccccaggaaagattcaggggagaggcccc
-20
-10
MetGluLeuThrAspLeuLeuLeuAlaAlaMetLeuLeuAlaValAlaArgLeuThrLeuSer
101 atacagggagccacttcagttagacaccctggccagaATGGAGCTGACTGATTTGCTCCTGGCGGCCATGCTTCTTGCAGTGGCAAGACTAACTCTGTCC
10
20
30
SerProValAlaProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisLeuLeuHisSerArgLeuSerGlnCysProAspValAspPro
201 AGCCCCGTAGCTCCTGCCTGTGACCCCAGACTCCTAAATAAACTGCTGCGTGACTCCCACCTCCTTCACAGCCGACTGAGTCAGTGTCCCGACGTCGACC
40
50
60
LeuSerIleProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnThrGluGlnSerLysAlaGlnAspIleLeuGlyAlaVal
301 CTTTGTCTATCCCTGTTCTGCTGCCTGCTGTGGACTTTAGCCTGGGAGAATGGAAAACCCAGACGGAACAGAGCAAGGCACAGGACATTCTAGGGGCAGT
70
80
90
100
SerLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGluProSerCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
401 GTCCCTTCTACTGGAGGGAGTGATGGCAGCACGAGGACAGTTGGAACCCTCCTGCCTCTCATCCCTCCTGGGACAGCTTTCTGGGCAGGTTCGCCTCCTC
110
120
130
LeuGlyAlaLeuGlnGlyLeuLeuGlyThrGlnLeuProLeuGlnGlyArgThrThrAlaHisLysAspProAsnAlaLeuPheLeuSerLeuGlnGlnLeu
501 TTGGGGGCCCTGCAGGGCCTCCTAGGAACCCAGCTTCCTCTACAGGGCAGGACCACAGCTCACAAGGACCCCAATGCCCTCTTCTTGAGCTTGCAACAAC
140
150
160
LeuArgGlyLysValArgPheLeuLeuLeuValGluGlyProThrLeuCysValArgArgThrLeuProThrThrAlaValProSerSerThrSerGln
601 TGCTTCGGGGAAAGGTGCGCTTCCTGCTTCTGGTAGAAGGTCCCACCCTCTGTGTCAGACGGACCCTGCCAACCACAGCTGTCCCAAGCAGTACTTCTCA
170
180
190
200
LeuLeuThrLeuAsnLysPheProAsnArgThrSerGlyLeuLeuGluThrAsnPheSerValThrAlaArgThrAlaGlyProGlyLeuLeuSerArg
701 ACTCCTCACACTAAACAAGTTCCCAAACAGGACTTCTGGATTGTTGGAGACGAACTTCAGTGTCACAGCCAGAACTGCTGGCCCTGGACTTCTGAGCAGG

FIG. 15B


210
220
230
LeuGlnGlyPheArgValLysIleThrProGlyGlnLeuAsnGlnThrSerArgSerProValGlnIleSerGlyTyrLeuAsnArgThrHisGlyProVal
801 CTTCAGGGATTCAGAGTCAAGATTACTCCTGGTCAGCTAAATCAAACCTCCAGGTCCCCAGTCCAAATCTCTGGATACCTGAACAGGACACACGGACCTG
240
250
260
AsnGlyThrHisGlyLeuPheAlaGlyThrSerLeuGlnThrLeuGluAlaSerAspIleSerProGlyAlaPheAsnLysGlySerLeuAlaPheAsn
901 TGAATGGAACTCATGGGCTCTTTGCTGGAACCTCACTTCAGACCCTGGAAGCCTCAGACATCTCGCCCGGAGCTTTCAACAAAGGCTCCCTGGCATTCAA
270
280
290
300
LeuGlnGlyGlyLeuProProSerProSerLeuAlaProAspGlyHisThrProPheProProSerProAlaLeuProThrThrHisGlySerProPro
1001 CCTCCAGGGTGGACTTCCTCCTTCTCCAAGCCTTGCTCCTGATGGACACACACCCTTCCCTCCTTCACCTGCCTTGCCCACCACCCATGGATCTCCACCC
310
320
330
GlnLeuHisProLeuPheProAspProSerThrThrMetProAsnSerThrAlaProHisProValThrMetTyrProHisProArgAsnLeuSerGlnGlu
1101 CAGCTCCACCCCCTGTTTCCTGACCCTTCCACCACCATGCCTAACTCTACCGCCCCTCATCCAGTCACAATGTACCCTCATCCCAGGAATTTGTCTCAGG
Thr
1201 AAACATAGcgcgggcactggcccagtgagcgtctgcagcttctcttcggggacaagcttccccaggaaggctgagaggcagctgcatctgctccagatgtt
1301 ctgctttcacctaaaaggccctggggaagggatacacagcactggagattgtaaaattttaggagctatttttttttaacctatcagcaatattcatcag
1401 agcagctagcgatctttggtctattttcggtataaatttgaaaatcactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
1501 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

FIG. 16

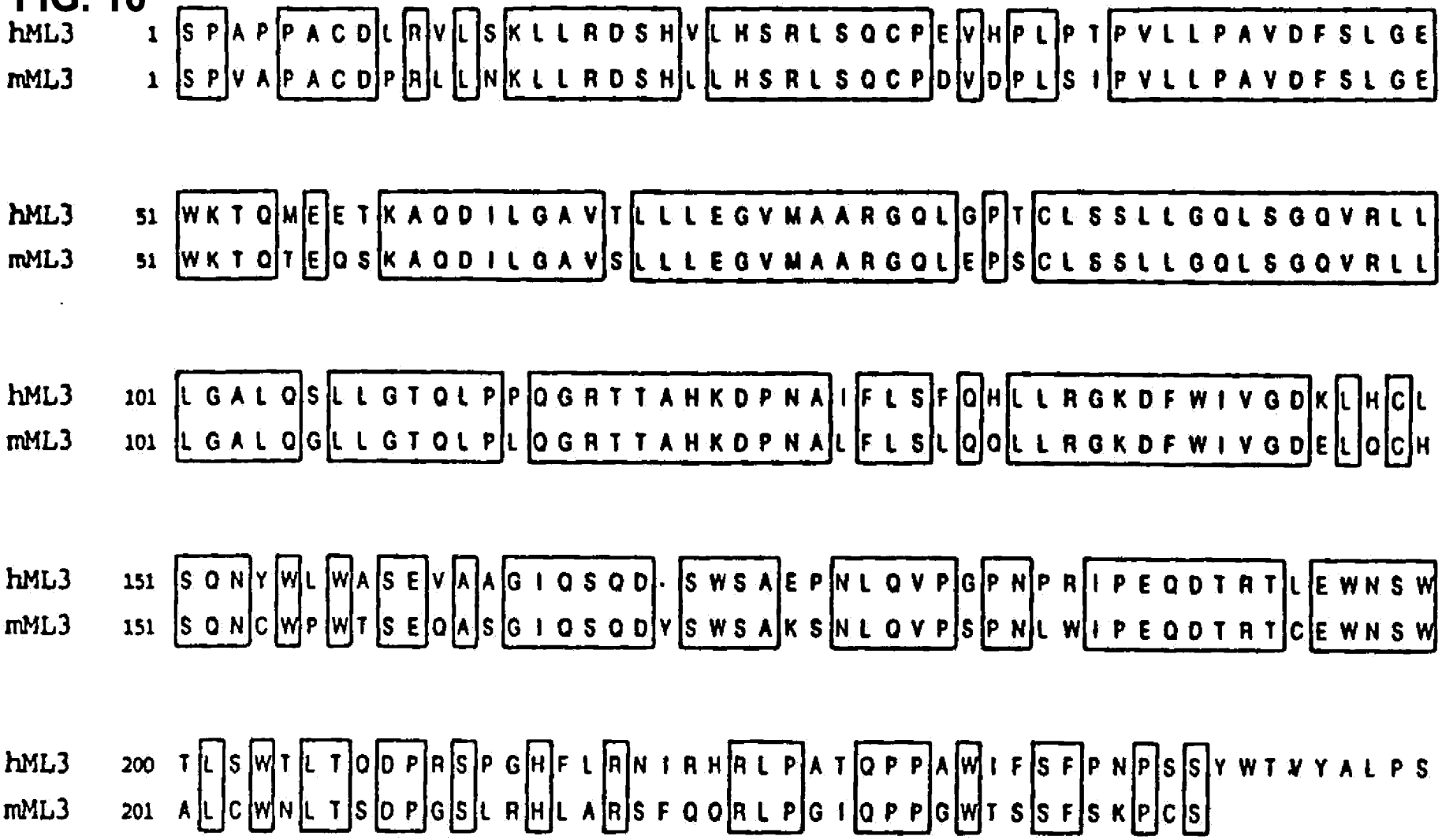


FIG. 17

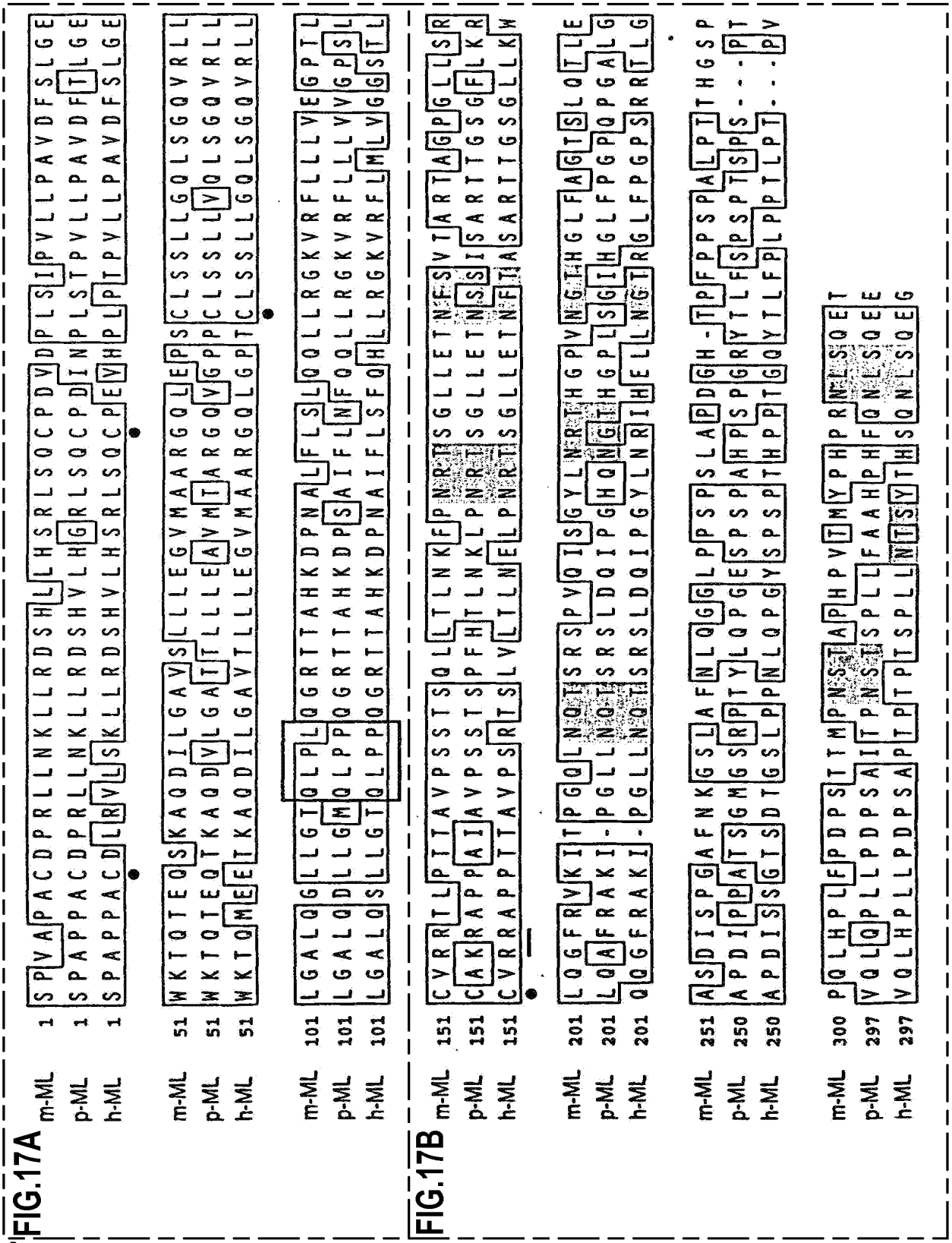


FIG. 17A

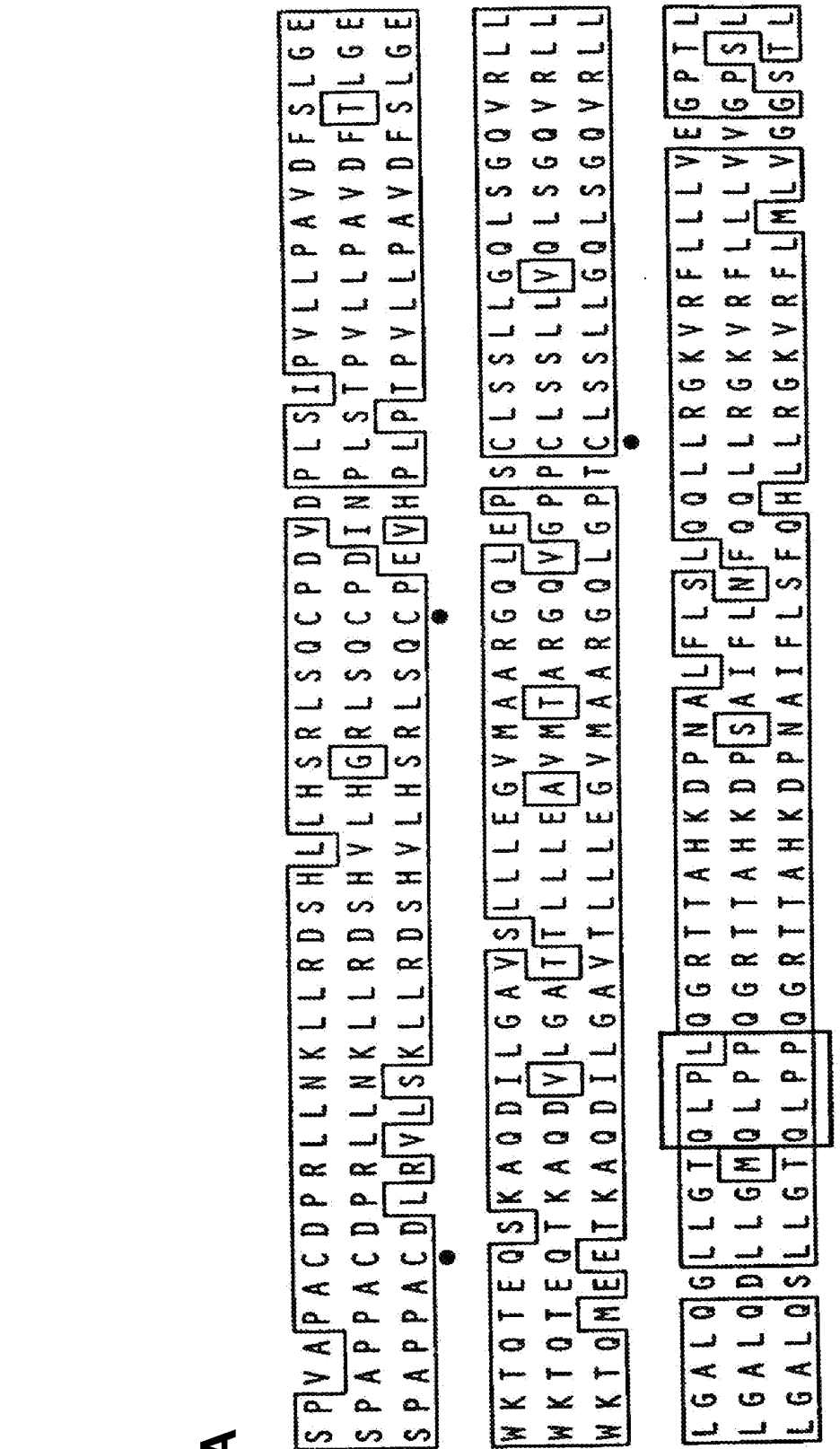

m-ML 1 SPVAPACDPRLLNKLLRDSHLLHSRLSQCPDVDPLSIPVLLPAVDFSLGE
p-ML 1 SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
h-ML 1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
m-ML 51 WKTQTEQSKAQDILGAVSLLLLEGVMAARGQLEPSCLSSLLGQLSGQVRLL
p-ML 51 WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
h-ML 51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
m-ML 101 LGALQGLLGTQLPLQGRTTAHKDPNALFLSLQQLLRGKVRFLLLVEGPTL
p-ML 101 LGALQDLLGMQLPPQGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
h-ML 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL

FIG.17B

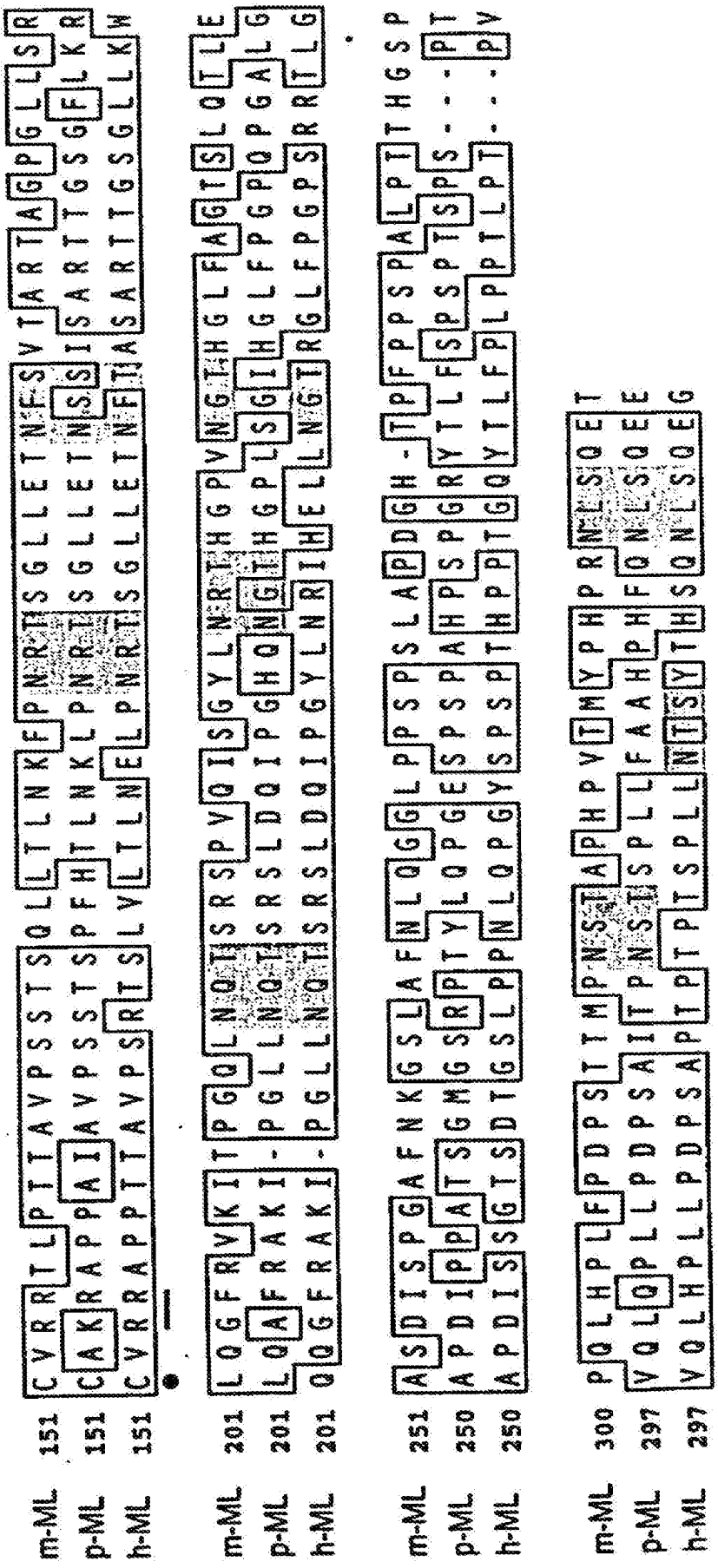

m-ML 151 CVRRTLPTTAVPSSTSQLLTLNKFPNRTSGLLETNFSVTARTAGPGLLSR
p-ML 151 CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
h-ML 151 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
m-ML 201 LQGFRVKITPGQLNQTSRSPVQISGYLNRTHGPVNGTHGLFAGTSLQTLE
p-ML 201 LQAFRAKI-PGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALG
h-ML 201 QQGFRAKI-PGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLG
m-ML 251 ASDISPGAFNKGSLAFNLQGGLPPSPSLAPDGH-TPFPPSPALPTTHGSP
p-ML 250 APDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSS---PT
h-ML 250 APDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPT---PV
m-ML 300 PQLHPLFPDPSTTMPNSTAPHPVTMYPHPRNLSQET
p-ML 297 VQLQPLLPDPSAITPNSTSPLLFAAHPHFQNLSQEE
h-ML 297 VQLHPLLPDPSAPTPTSPLLNTSYTHSQNLSQEG

FIG. 18

FIG.18A

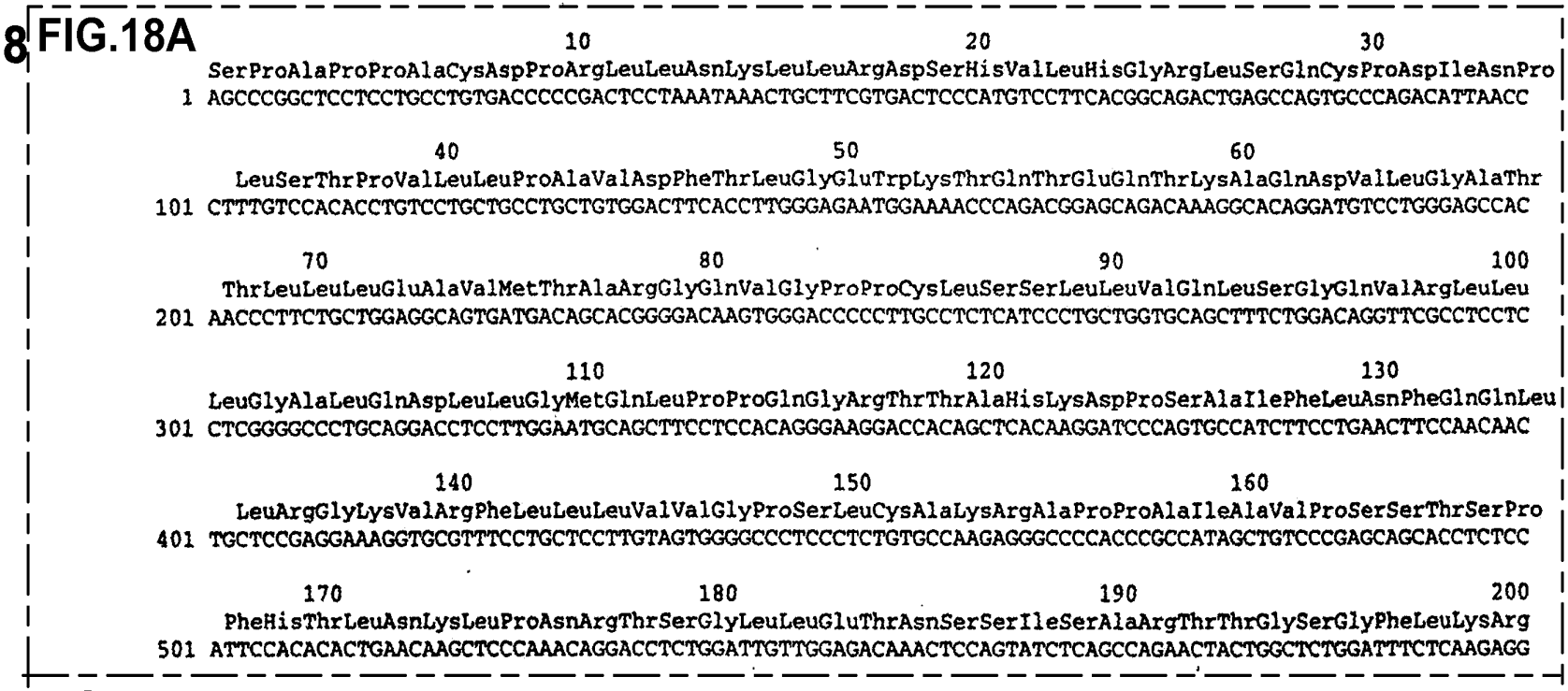


FIG.18B

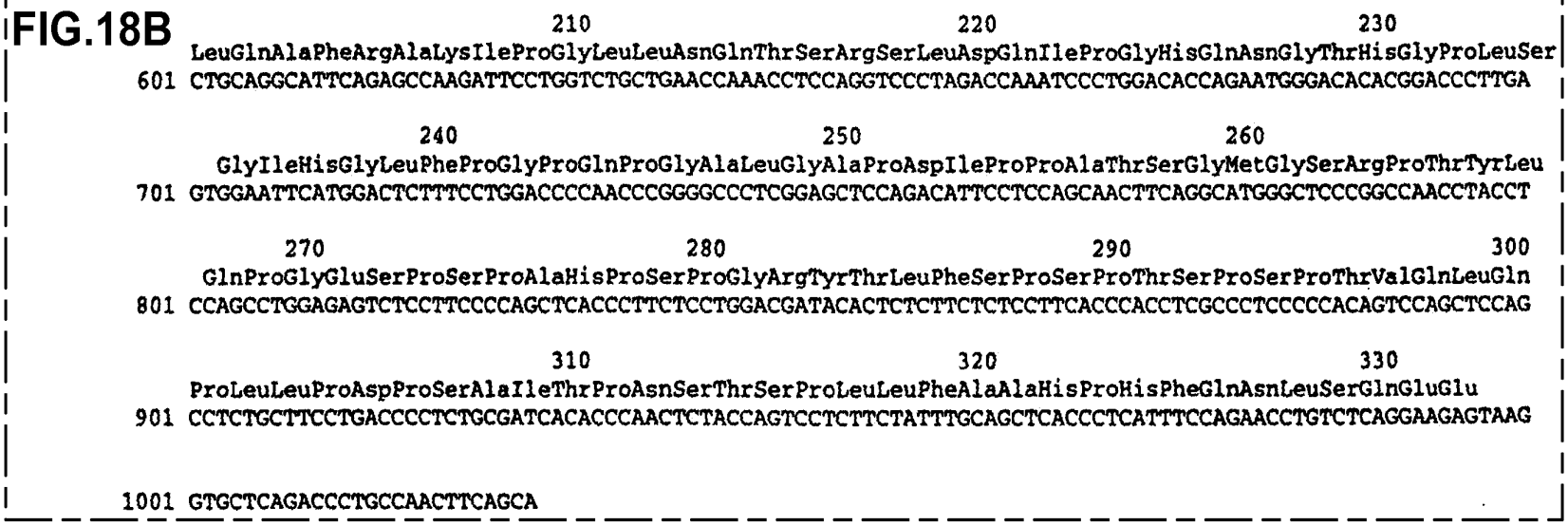


FIG.18A


10 20 30
SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
1 AGCCCGGCTCCTCCTGCCTGTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCAGACATTAACC
40 50 60
LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
101 CTTTGTCCACACCTGTCCTGCTGCCTGCTGTGGACTTCACCTTGGGAGAATGGAAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC
70 80 90 100
ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
201 AACCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGGACCCCCTTGCCTCTCATCCCTGCTGGTGCAGCTTTCTGGACAGGTTCGCCTCCTC
110 120 130
LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeu
301 CTCGGGGCCCTGCAGGACCTCCTTGGAATGCAGCTTCCTCCACAGGGAAGGACCACAGCTCACAAGGATCCCAGTGCCATCTTCCTGAACTTCCAACAAC
140 150 160
LeuArgGlyLysValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerPro
401 TGCTCCGAGGAAAGGTGCGTTTCCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCC
170 180 190 200
PheHisThrLeuAsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArg
501 ATTCCACACACTGAACAAGCTCCCAAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGG

FIG. 18B

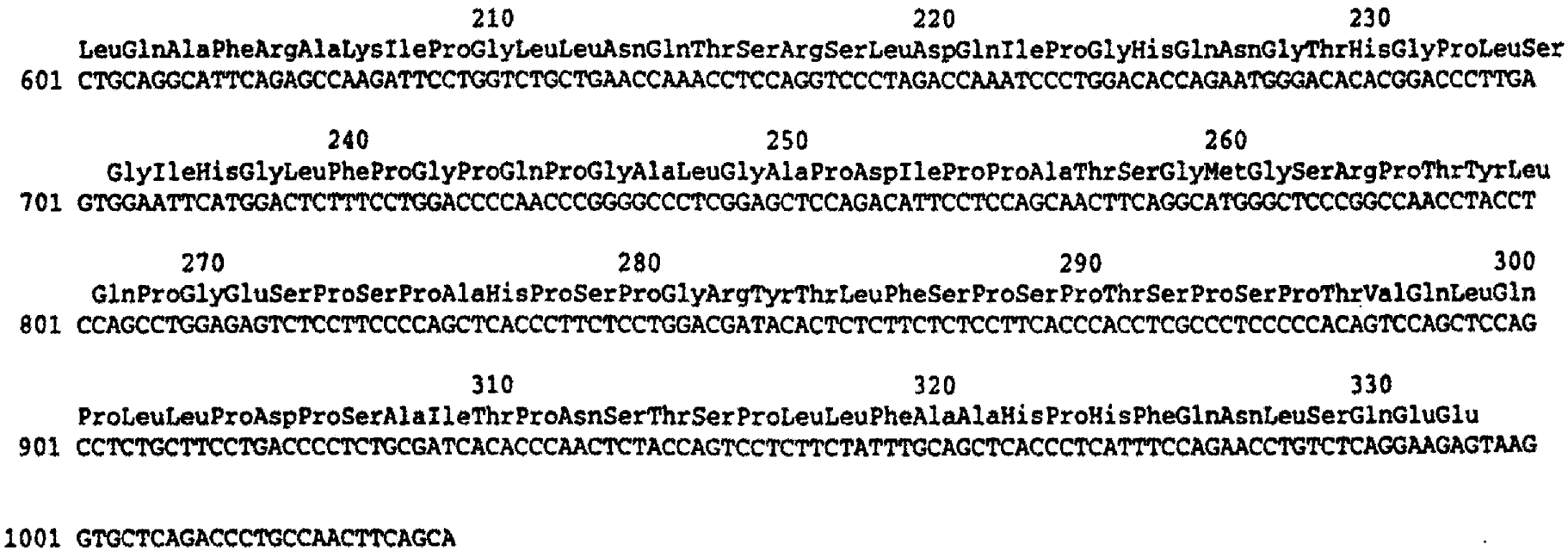

210
220
230
LeuGlnAlaPheArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSer
601 CTGCAGGCATTCAGAGCCAAGATTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTAGACCAAATCCCTGGACACCAGAATGGGACACACGGACCCTTGA
240
250
260
GlyIleHisGlyLeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeu
701 GTGGAATTCATGGACTCTTTCCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCT
270
280
290
300
GlnProGlyGluSerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGln
801 CCAGCCTGGAGAGTCTCCTTCCCCAGCTCACCCTTCTCCTGGACGATACACTCTCTTCTCTCCTTCACCCACCTCGCCCTCCCCCACAGTCCAGCTCCAG
310
320
330
ProLeuLeuProAspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
901 CCTCTGCTTCCTGACCCCTCTGCGATCACACCCAACTCTACCAGTCCTCTTCTATTTGCAGCTCACCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAG
1001 GTGCTCAGACCCTGCCAACTTCAGCA

FIG. 19

FIG. 19A

FIG.19B

FIG. 19A

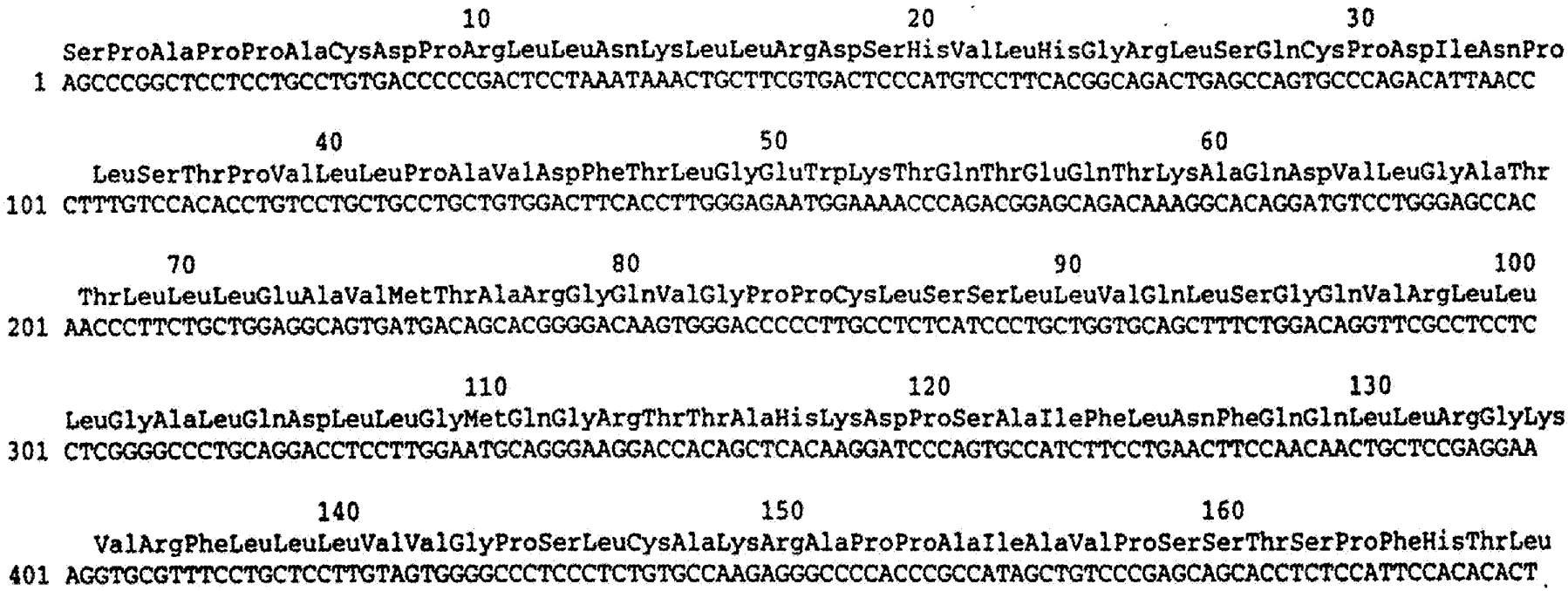

10 20 30
SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
1 AGCCCGGCTCCTCCTGCCTGTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCAGACATTAACC
40 50 60
LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
101 CTTTGTCCACACCTGTCCTGCTGCCTGCTGTGGACTTCACCTTGGGAGAATGGAAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC
70 80 90 100
ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
201 AACCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGGACCCCCTTGCCTCTCATCCCTGCTGGTGCAGCTTTCTGGACAGGTTCGCCTCCTC
110 120 130
LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeuLeuArgGlyLys
301 CTCGGGGCCCTGCAGGACCTCCTTGGAATGCAGGGAAGGACCACAGCTCACAAGGATCCCAGTGCCATCTTCCTGAACTTCCAACAACTGCTCCGAGGAA
140 150 160
ValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerProPheHisThrLeu
401 AGGTGCGTTTCCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCCATTCCACACACT

FIG. 19B

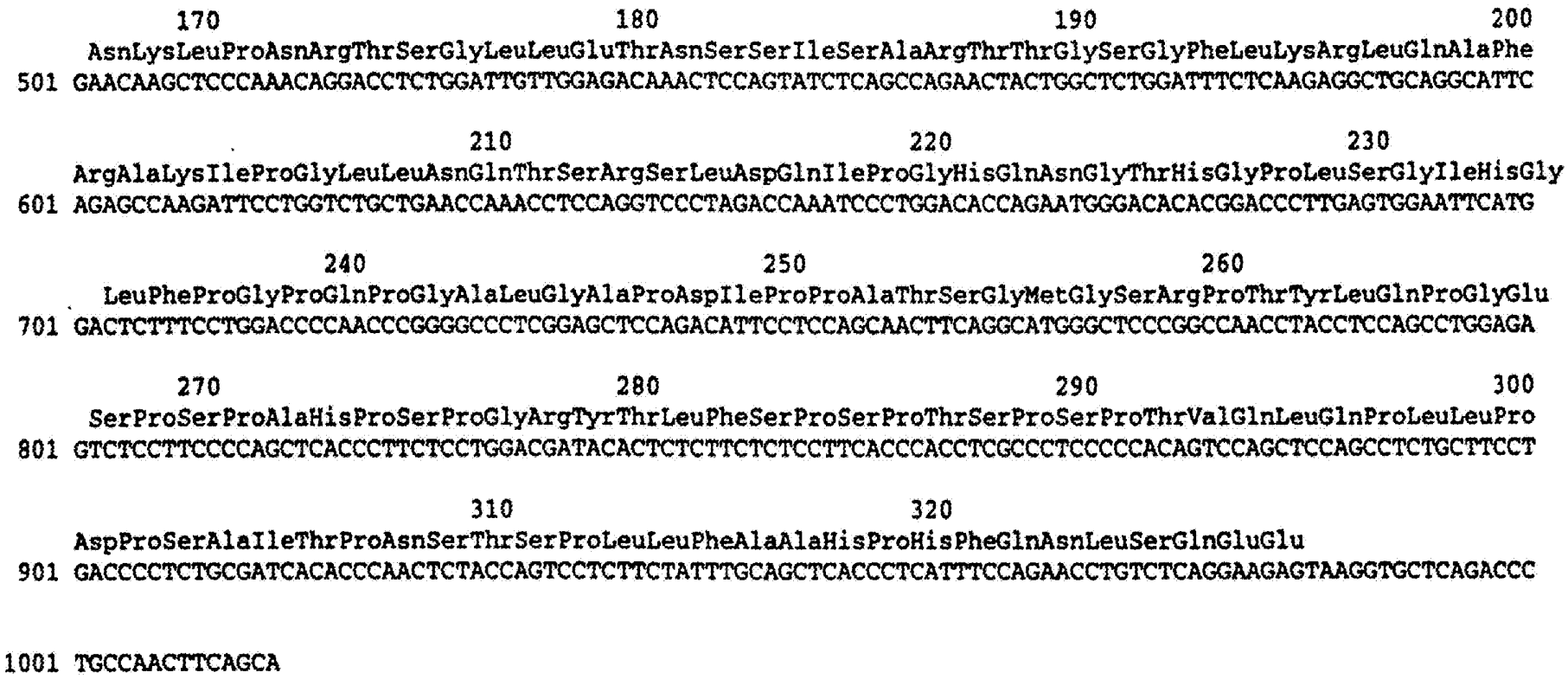

170 180 190 200
AsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArgLeuGlnAlaPhe
501 GAACAAGCTCCCAAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGGCTGCAGGCATTC
210 220 230
ArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSerGlyIleHisGly
601 AGAGCCAAGATTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTAGACCAAATCCCTGGACACCAGAATGGGACACACGGACCCTTGAGTGGAATTCATG
240 250 260
LeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeuGlnProGlyGlu
701 GACTCTTTCCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCTCCAGCCTGGAGA
270 280 290 300
SerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGlnProLeuLeuPro
801 GTCTCCTTCCCCAGCTCACCCTTCTCCTGGACGATACACTCTCTTCTCTCCTTCACCCACCTCGCCCTCCCCCACAGTCCAGCTCCAGCCTCTGCTTCCT
310 320
AspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
901 GACCCCTCTGCGATCACACCCAACTCTACCAGTCCTCTTCTATTTGCAGCTCACCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAGGTGCTCAGACCC
1001 TGCCAACTTCAGCA

FIG. 20

FIG.20A

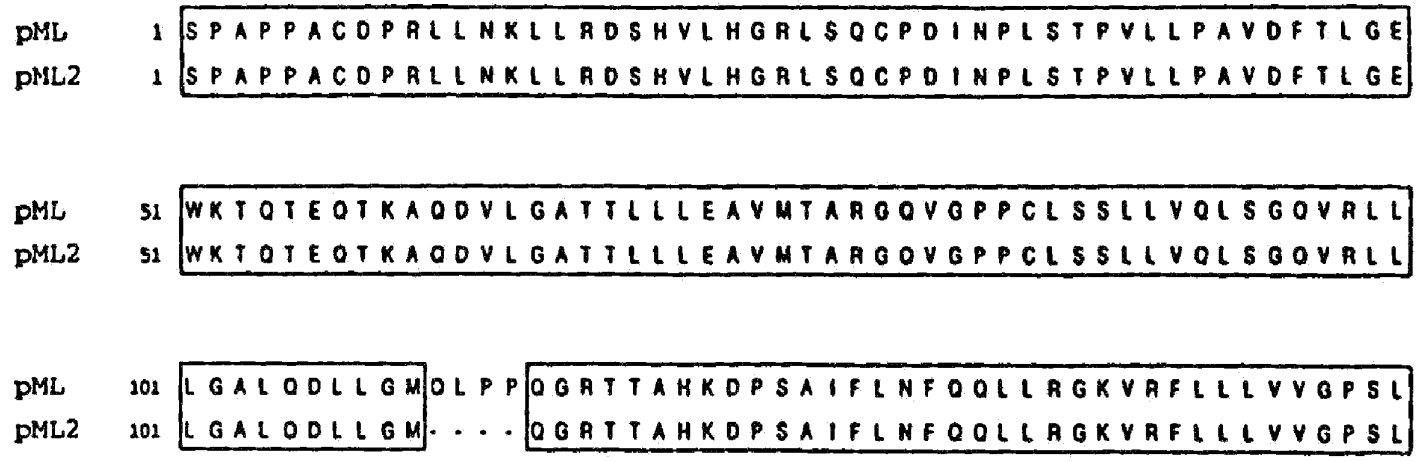


FIG.20B

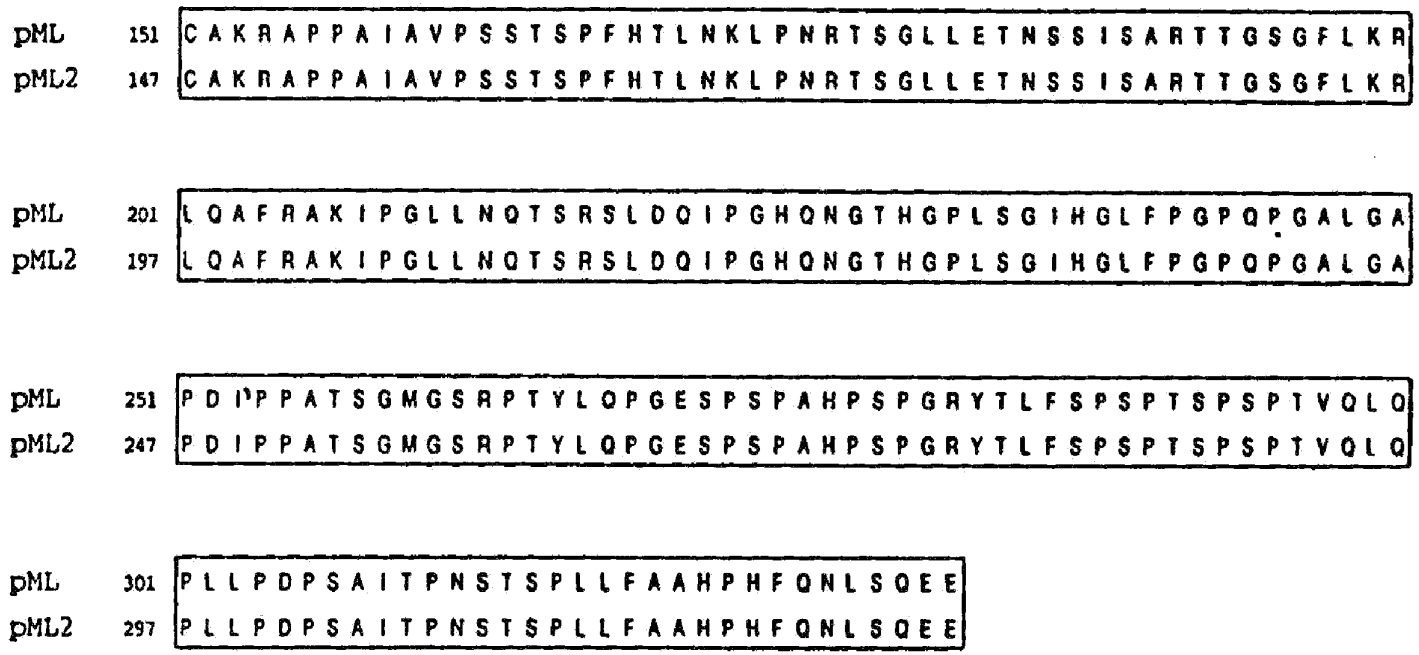


FIG. 20A

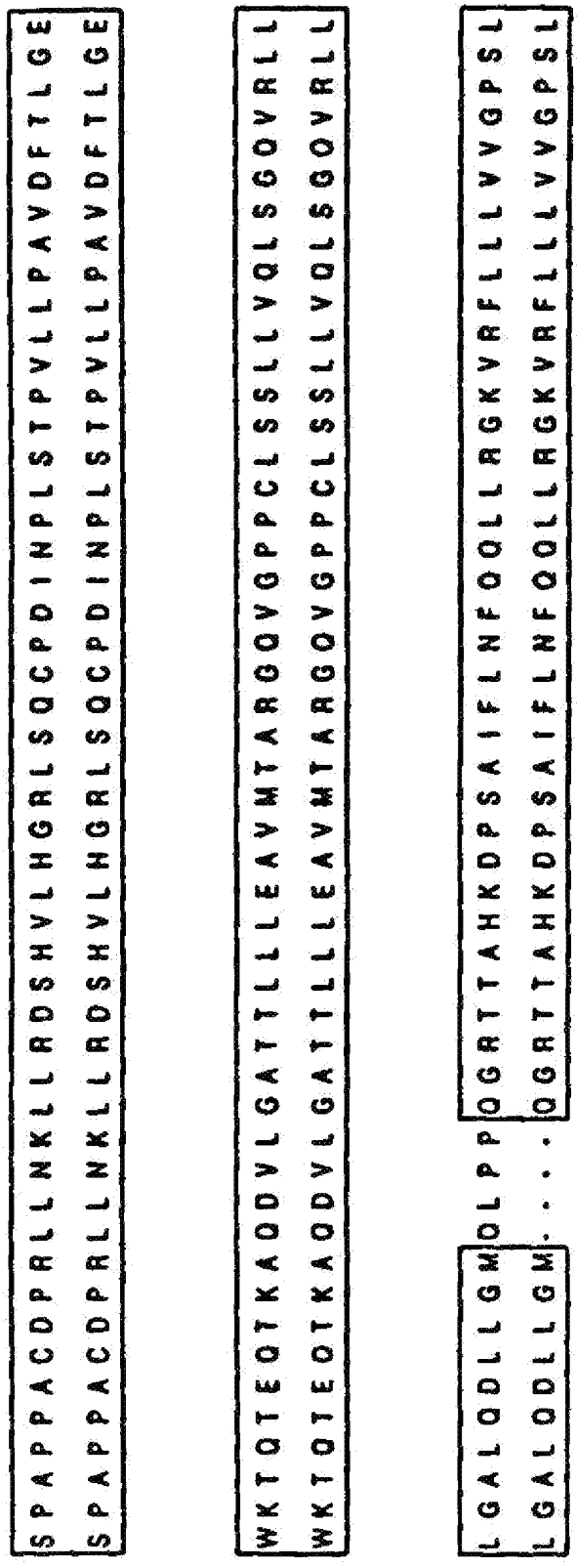
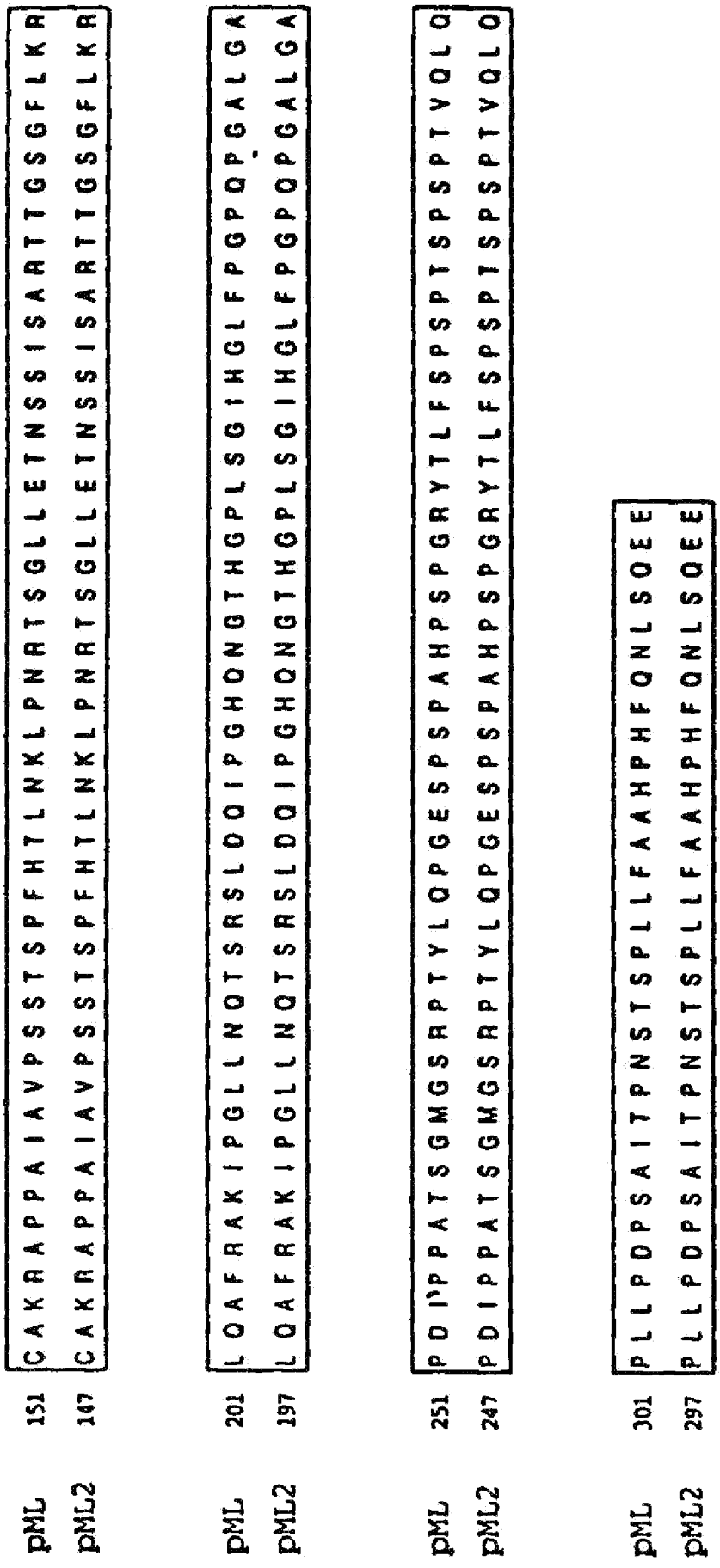

pML 1 SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
pML2 1 SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
pML 51 WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
pML2 51 WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
pML 101 LGALQDLLGMQLPPQGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
pML2 101 LGALQDLLGM. . . QGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL

FIG. 20B


pML 151
CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
pML2 147
CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
pML 201
LQAFRAKIPGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALGA
pML2 197
LQAFRAKIPGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALGA
pML 251
PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ
pML2 247
PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ
pML 301
PLLPQPSAITPNSTSPLLFAAHPHFQNLSQEE
pML2 297
PLLPQPSAITPNSTSPLLFAAHPHFQNLSQEE